Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein. Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 22, 2005, 05:57:23 ; Search time 26.813 Seconds (without alignments) 1008.352 Million cell updates/sec

US-10-662-429-2 1478 ritle:

Perfect score:

1 MAMMEVQGGPSLGQTCVLIV......NEHLIDMDHEASFFGAFLVG Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tumor necrosis fac lymphotoxin alpha tumor necrosis fac tumor necrosis fac Fas ligand - mouse Fas ligand - human fas ligand - rat CD40 ligand - bovi CD40 ligand - huma tumor necrosis fac lymphotoxin - bovi tumor necrosis fac tumor necrosis fac tumor necrosis fac CD40 ligand - mous tumor necrosis fac umor necrosis fac ymphotoxin-beta -NRNA maturase b14 tumor necrosis tumor necrosis necrosis necrosis Description tumor tumor QWMSN JU0029 QWHUX JH0529 S06192 B27303 S52715 I49139 A49266 S53090 I53476 S21738 S17289 S24642 I54490 S24641 QWHUN S12606 S22052 JQ1344 A53062 В Query Match Length 189.5 186 177.5 164 147.5 121 115.5 114 113.5 113.5 112.5 111.5 109 107 100 134.5 133 131.5 131 130.5 129.5 127.5 125.5 123.5 123.5 141 Result No.

tumor necrosis fac	protein kinase, pr	DNA ligase homolog	hypothetical prote	hypothetical prote	hypothetical prote	chromodomain helic	heat shock transcr	cardiac muscle fac	myosin-light-chain	. serine/threonine k	activin receptor-1	hypothetical prote	hypothetical prote	NBS-LRR type resis	alpha-N-arabinofur
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81168	F9512	T14707	T1501	G921 (T184	T2305	A3159	T2909	3N058	JC2491	A5344	T4057	E9663	T0303	B59296
2 \$1168	2 F9512	2 T1470	2 T1501	2 G951	2 T184	2 T2305	1 A3159	2 T2909	2 JN058	2 JC249	2 A5344	2 T4057	2 E9663	2 T0303	2 B5929
7	7	N	~	~	~	N	833 1 A3159	N	~	~	~	~	N	- N	7
233 2	448 2	345 2	365 2	455 2	4981 2	1465 2	н	1538 2	1176 2	502 2	502 2	1284 2	907 2	313 2	328 2 E
233 2	448 2	6.4 345 2	6.4 365 2	6.4 455 2	6.4 4981 2	6.4 1465 2	833 1	6.3 1538 2	6.2 1176 2	6.1 502 2	6.1 502 2	6.1 1284 2	6.1 907 2	6.1 313 2	6.0 328 2 E

ALIGNMENTS

RESOLT 1 AS3062 Fas Isga C;Specie C;Date: C;Access	A55062 Fas ligand - mouse C:Species: Mus musculus (house mouse) C:Apecio (0-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C:Accession: A53062 R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell A; Tit A; Refi A; Acc A; Acc A; Mol A; Res A; Cro	Cell 76, 969-976, 1994 A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A;Reference number: A53062; MUID:94185175; PMID:7511063 A;Accession: A53062 A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-279 <tak> A;Cross-references: UNIPROT:P41047; GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565</tak>
Oue: Besi Mate	Query Match Best Local Similarity 25.8%; Pred. No. 1.7e-08; Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;
ò a	83 QLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSBNSK 142 : ; ; ; ;
රු සි	143 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSGTYPRPGEEIKENTKN 202
රු සි	203 DKQMVQYIY-KYTSYPDPILLMKSAR-NSGWSKDAEYGLYSIYQGGIPELKENDRIFVSV 260 ::::: :: :: :: 202 NQPLNHKYYMRNSKYPEDLVLMEEKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNI 259
ò a	261 TNEHLIDMDHEASFFGAF 278 : : : : 260 SQLSLINPEESKTFFGLY 277

RESULT 2

Fas ligand - human Cispecies: Homo sapiens (man) Cjate: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004 CjAccession: I38707; JC2240; S57565; I38554 R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S. Hr. Immunol. 6, 1567-1574, 1994 A;Title: Human Pas ligand: gene structure, chromosomal location and species specificity. A;Reference number: I38707; MUID:95127560; PMID:7826947

amphotropic murine tumor necrosis fac

probable membrane

A;Accession: 138707 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-281 (kEEs> A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:95954

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A; Molecule type: mRNA
A; Residues: 1-261 < MER>
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A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R;Suda, T.: Takahashi, T.: Golstein, P.: Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266
A;Reference number: A49266
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-278 < SUD>
A;Residues: 1-278 < SUD>
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C;Reywords: glycoprotein; transmembrane protein
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                                                                                                                                                                                                   Rischarzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: 857865
A;Accession: 857865
A;Status: preliminary
A;Residues: 1-281 «SCH»
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
B;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; C.
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: 138554; MUID:95105731; PMID:7528780
                                                                                                                                                                                A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biocham. Biophys. Rest. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection. A;Reference number: JC2340; MUID:95071350; PMID:7980502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;80-102/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNS-----CWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAV---TYVYFTNELKQMQDKYSKSGIACFLKE 60
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                      A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
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CD40 ligand - human
NiAlternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
NiAlternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: S28017; JH0793; S2664; S28852; I53476; S25684; S30593
C;Accession: S28017; JH0793; Z26644; S28852; I53476; S25684; S30593
B;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; b
BMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g73257
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                                                                                                                                                                                                                                                                                                                                                                   163 YGTALISGVKYKKGGLVINBAGLYFVYSKVYFRGQ-----SCNSQPLSHKVYMRNFKYP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276
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                                                                                                                                                                                                                                    ------ EWEDT- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 YWDPNDEESMNS--PCWQVKWQLRQLVRKMILRTSEBTISTVQEKQQNISPLVRERGPQR 121
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C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S33090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the RMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNPA and TNFB.
A;Reference number: S53090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VATGPPVSMK-IFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLHBDFVFMK---T
                                                                                                                                                                                                                                                                                                                  159 SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 DPILLAMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
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                                                                                 Gaps
                                                                             29;
    278;
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11.1%; Score 164; DB 2; Length 26
Best Local Similarity 25.9%; Pred. No. 2.3e-06;
Matches 72; Conservative 52; Mismatches 114; Indels
    Length
                                                                                 Indels
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    DB 2;
                                                                                                                                                                                                                121 VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL-
Query Match
12.0%; Score 177.5; DB 3
Best Local Similarity 27.5%; Pred. No. 1.8e-07,
Matches 50; Conservative 39; Mismatches 64
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us-10-662-429-2.rpr

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Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
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Cypecies: Mus musculus (house mouse)
Cypecies: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cypate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cypeciesion: S21738
Cypecies: 321738
Nature 357, 80-82, 1992
Nature 357, 80-82, 1992
AyTitle: Molecular and biological characterization of a murine ligand for CD40.
AyReference number: S21738
AyAccession: S21738
AyAccession: S21738
AyMulD:92244364; PMID:1374165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-234 <ITO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD40 ligand - mouse
                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A25451
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Matches
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A;Reference number: $28017; WUD: 93049181; PMID:1385114
A;Accession: $28017
A;Molecule type: mBNA
A;Residues: 1-261 cHOL-
A;Cross-references: UNIPROT: P29965; EMBL: Z15017; NID: 938483; PIDN: CAA78737.1; PID: 938484
A;Residues: 1-261 cHOL-
A;Cross-references: UNIPROT: P29965; EMBL: Z15017; NID: 938483; PIDN: CAA78737.1; PID: 938484
R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
A;Title: Recombinant human C040 ligand stimulates B cell proliferation and immunoglobuli
A;Reference number: JH0793; WUD: 93094757; PMID: 1281209
A;Rolecule type: mRNA
A;Residues: 1-261 cSPR-
A;Cross-references: GB: K67878; NID: 938411; PIDN: CAA48077.1; PID: 938412
A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
A;Experimental source: peripheral blood T-cell
B;Cross-references: GB: K67878; NUD: 93076854; PMID: 1280226
A;Title: Cloning of TRAP, a ligand for C040 on human T cells.
A;Reference number: S26694
A;Recession: S26694
A;Recession: S26694
A;Recession: S26694
A;Residues: 1-261 cGRA-
A;Cross-references: EMBL: X68550; NID: 937269; PIDN: CAA48554.1; PID: 937270
R;Gauchat, JF: Ambry, J-P: Mazzei, G: Life, P.; Jomotte, T.; Elson, G: Bonnefoy, J.
FEBS Lett. 315, 255-266
A;Reference number: S28852; MUD: 93188085; PMID: 7678552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: $28852
A; Molecule type: mRNA
A; Residuae: 1-261 <GAU>
A; Residuae: 1-261 <GAU>
A; Cross-references: EMBL: L07414; NID: 9180123; FIDN: AAA35662.1; PID: 9180124
A; Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EESMN-SPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYIY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ISEASSKTTSVL----QW--AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQTYFRFQEEIKENT-----KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 AQVTFCSNREASSQAPFIASLCLKSPGRFER--------ILLRAANTHSSAKPC-- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A25451
tumor necrosis factor alpha precursor - rabbit
tumor necrosis factor alpha
N/Alternate names: cachectin; TNF alpha
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Species: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 VLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP----ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A map position: Xq26-Xq26
C; Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%; Score 147.5; DB 2; Length 261; 23.7%; Pred. No. 5.7e-05; ive 51; Mismatches 99; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:120632; OMIM:308230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: CD40LG; HIGM1; IMD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 23.74 tes 66; Conservative
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Matches
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Ritto, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajinara, J.; Kiyota, T.; nayasui, n. DNA S, 149-156, 1986
A,Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabt A,Reference number: A25454; MUID:86219711; PMID:3519137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B. MS, S.; 157-165, 1986 A; Mallace, R.B. A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor. A;Reference number: A25451; MUID:86219712; PMID:3519138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-234 <IT2>
A; Note: this sequence differs from that shown in having a Gln inserted between residues .
B; Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A; Title: Structural analysis of the rabbit TNP locus, containing the genes encoding TNP-i
A; Reference number: JH0309; MUID:91065534; PMID:2249779
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A, Molecule type: DNA
A, Molecule to the type: Molecule type: Molecul
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Introns: 62/3; 78/1; 93/1
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Best Local S:
Matches 61
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A,Cross-references: UNIPROT:P27548; EMBL:X65453; NID:950351; PIDN:CAA46448.1; PID:950352 (Keywords: glycoprotein; transmembrane protein F;23-46/Domain: transmembrane #status predicted <TWM> F;23-46/Domain: extracellular #status predicted <TWM> F;47-260/Domain: extracellular #status predicted <EXT> F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor beta precursor - pig
CiSpecies: Sus scrofa domestica (domestic pig)
CiDate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CiAccession: S17289
R:Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:1874444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: S17289
A,Molecule type: DNA
A,Residues: 1-204 <KUH>
A,Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                   75 S--PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGR 132
                                                                                                                                                                                                                                                                                                                                                                                                      133 SNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                  191 RFQEEIKENTKNDKQMVQYIYKYTSYPDPILLAMKSARNSCWSKDAEYGLYSIYQGGIFEL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSNRE----PSSQRPFIVGLWLKPSIGSERILLKAANTHSSSQLCEQ--QSVHLGGVFEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 STVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 VLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMN
                                                                                                                                                                                    Gaps
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                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.1%; Score 134.5; DB 1; Length 204; Best Local Similarity 24.7%; Pred. No. 0.00051; Matches 46; Conservative 31; Mismatches 76; Indels 33
                                                                                                                                      Score 141; DB 2; Length 260;
Pred. No. 0.0002;
                                                                                                                                      Query Match 9.5%; Score 141; DB 2; Length 26(
Best Local Similarity 23.5%; Pred. No. 0.0002;
Matches 59; Conservative 50; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 KENDRIFVSVT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QAGASVFVNVT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 SFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 VFFGAF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 32/3; 68/1
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A.Cross-references: UNIPROT: P23563; EMBL:XS4001; NID:92135; PIDN:CAA37949.1; PID:92136 R; Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U. Gene 102, 171-178, 1991
A.F.Itle: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal) A.Reference number: S17289; MUID:91340150; PMID:1874444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-232 «KUH>
A; Residues: 1-232 «KUH>
A; Cross -references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A; Notes: the authors translated the codon GAG for residue 202 as Gly
R; Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A; Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fac
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Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myris
1-77/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S18965
A;Molecule type: mRNA
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
B;Pauli, U.; Beutler, B.; Peterhans, E.
R;Pauli, U.; Beutler, B.; Peterhans, E.
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A;Reference number: 146659; MUID:90034181; PMID:2478420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 KGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
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tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 10-Sep-1999 #sequence 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S12606; 817290; S18965; 146659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Ritle: Gene sequence of porcine tumor necrosis factor alpha.
A;Ritle: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Molecule type: DNA
A;Residues: 1-232 <DNBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 --VIGPQKEEFPAGPL------SINPLAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 146659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;14-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 ---DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
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ilarity 21.3%; Pred. No. 0.00082;
Conservative 40; Mismatches 100
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tunor necrosis factor alpha precursor - bovine C.Species: Bos primiganius taurus (cattle) C.Species: Bos primiganius taurus (cattle) C.Species: Bos primiganius taurus (cattle) C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C.Accession: 146047; S24642 R.C.Iduts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L. Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L. Clonits and characterization of the tandemly arranged bovine lymphotoxin and A.Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and A.Reference number: 146046; MUID:94083525; PMID:8260599
                                                                                                                                                                                                                                                                                                                                                 60 EDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 ---KEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVR 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 IHEKGFYYIYSQTYFRFQBEIKENTKNDKQMVQYIYK--YTSYPDPILLMKSARNSC--- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: Q06599; EMBL: Z14137; NID: 9796; PIDN: CAA78511.1; C; Genetics:
                                                                                                                                                                                                                                 8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFL-----K
                                                                                                                                                                                                                                                                                           22 GGPQGSRRCLCLSLFSFLL----VAGATTLF----------CLLHFGVIGPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 LSEKAGGPQGSRSCLCLSLFSFLL----VAGATTLF-----------------CLLHFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ----NKPVAHVVA-----DINSPGQLR------WWDSYANALMANGVKLEDNQLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aintrons: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane |
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;81/Binding bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;19,20/Binding site: myristate (Lys) (covalent) #status predicted F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted F;146-178/Disulfide bonds: #status predicted
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                                                                                                                  Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                       61 EEQL---PNAFQSIN-PLAQT-----LRSSSRTPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 130.5; DB 1;
20.3%; Pred. No. 0.0013;
... w.emarches 95;
                                                                                                               , DB 1;
0.0012;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 20.3%; Pred. No. 0.001;
Matches 59; Conservative 43; Mismatches
                                                                                                                                                                        40; Mismatches
                                                                                                                  8.9%; Score 131;
20.8%; Pred. No. 0
                                                                                                                                                                        60; Conservative
                                                                                                                                       Best Local Similarity
Matches 60; Conserv
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                                                                                                                  Query Match
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                                                                                                                                                                                                                                 R;Sanjanwala, M; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Residues: 1-233 <SAN>
A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:G38159; PIDN:CAA44068.1; PID:G38160
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A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C;Comment: This protein is an important proximal mediator of endotoxemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mem
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R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis A;Accession: JQ1344; MUID:92084125; PMID:1748301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: tumor necrosis factor
C;Reywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                      09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ALPKKTGGPQGSRRCLFLSLFSFLLVAGATTLFCLLHFGVIGPQREEFPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNBLKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation; transmembrane
F;19,20/Binding site: myristete (Lys) (covalent) #status predicted
F;18/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 131.5; DB 1; Length 233; 19.2%; Pred. No. 0.0011;
   228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DP----SLISPLAQA------VRSSSRTPS----SLISPLAQA
                                                                                                                                                                                                      #text_change
   EGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                     C;Species: Papio sp. (baboon)
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S22052
R;Sanjamala, M.; Edwards, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Mismatches
                                                                                                                                             - baboon
                                                                                                                                                necrosis factor alpha precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 62/3; 78/1; 94/1
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PID:9798

protein

13;

Gaps

22

82

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tumor necrosis factor alpha precursor [validated] - human N;Alternate names: cachectin; TNFA C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Daternate names: Sabug-1985 #sequence_revision 28-Aug-1985 #text change 09-Jul-2004 C;Accession: A93585, S36153; A9351; A44189; B61478; I53311; S62610; I54522; A01646; B237 R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D. Nucleic Acids Res. 13, 6361-6373, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chron:
Reference number: A93585; MUID:86016093; PMID:2995927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: UNIPROT: P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P1|R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka, Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a A;Reference number: S36152; MUID:93272029; PMID:8499947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-233 <IRI>
A; Cross-references: EMBL:Z15026; NID:G37211; FIDN:CAA78745.1; FID:G37212
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R; Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A..,
Nature 312, 724-729, 1984
A; Fitle: Human tumour necrosis factor: precursor structure, expression and homology to 1).
A; Reference number: A93351; MUID:85086244; PMID:6392892
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A; Residues: 1-233 < PEN>
A; Residues: 1-233 < PEN>
A; Residues: 1-233 < PEN>
A; Cross-references: GB.X02910; GB.X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Cross-references: GB.X02910; GB.X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc; R; Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; N Science 228, 149-154, 1985
A; Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A; Reference number: A44189; MUID:85142190; PMID:3856324
A; Residues: 1-62. 'S, 64-233 < WAN>
A; Ritle: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A; Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A; Reference number: A61478; MUID:88301617; PMID:2841543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 83-102;109-119;121-128, X', 130-131;142-144, X', 146, XXX', 150-152;159-174;180.,
B; Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, F. Bur. J. Biochem. 152, 515-522, 1985
A; Title: Molecular cloning and expression of human tumor necrosis factor and comparison value ference number: 153311; MUID: 86030296; PMID: 3932069
                                                                                                                                                                                   89 -----HGF----SLSNNSLLVPTSGLYFVYSQVVFSGRGCFPRATPTPLYLAHEVQ 135
                                                                                                                                                                                                                                                                                                                                                    212 KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD 269
                                           88
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----DRAFLR--
                                                                                                                              152 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY
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40 TPSAAQPAHQQL-PTPFTRGTLKPAAHLVGDPSTQDSLRWRANT-
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A,Molecule type: DNA
A,Residues: 1-233 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 HEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 PSSVFFGAF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA; Residues: 1-233 <NED>
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Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
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C;Genetics:
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: 146046; 224641
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and hareference number: 146046; MUID:94083525; PMID:8260599
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 151
                                                                                                                                                                                                                                                                                           tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
    ---WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                TPEWA-EAKPWYEPIYQGGVFQLEKGDRLSAEINLPDYLDYAESGQVYFG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Reywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate [Lys] (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

8.8%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0016;
Matches 45; Conservative 39; Mismatches 75; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
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8.6%; Score 127.5; DB 1; Length 2
Best Local Similarity 24.9%; Pred. No. 0.002;
Matches 47; Conservative 29; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
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A; Molecule type: DNA A; Residues: 1-204 <CL2>

Introns: 32/3; 68/1

274 -FFG 276 VYFG 231

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lymphotoxin - bovine

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C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimental 
C; 1-76-100 product: tumor necrosis factor status experimental 
F; 77-23/ Product: tumor necrosis factor status experimental
F; 19, 20/Binding site: myristate (Lys) (covalent) #status experimental
F; 81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F; 145-177/ Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                R.D.Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
Affile: A polymorphic variation in a putative regulation box of the TNFA promoter region A; Reference number: 154522; MUID:94102809; PMID:7903959
A; Accession: 154522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:S68530; NID:g544751
R; Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
G. Exp. Med. 176, 1053-1062, 1992
A; Title: Wyristyl acylation of the tumor necrosis factor alpha precursor on specific lys A; Reference number: A59163; MUID:93018820; PMID:1402651
A; Contents: annotation; identification of myristylated lysines
R; Aggarwal, B.B.; Kohr, W.J.; Hass, P.B.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and -beta (lymphotoxin) are products of different genes closely ut are produced by different cell types and have different induction kinetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7,7391. Chem. 260, 2345-2354, 1985
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 DSYWDPNDEESMNSPCWOVKWQLRQLVRKMILRTSEETISTVOEKOONISPLVRERGPOR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ------DLSLISPLAQA-----DKSSSRTPS-----DK 87
                                    A; Experimental source: U-937 cells
R; Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A; Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A; Reference number: S62610; MUID:96202967; PMID:8631363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
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A; Cross-references: GB: M26331; NID: 9339763; PIDN: AAA36758.1; PID: 9339764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
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8.5%; Score 125.5; DB 1; Length 233;
Best Local Similarity 17.8%; Pred. No. 0.0036;
Matches 51; Conservative 52; Mismatches 99; Indels 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation; disulfide bond
                                                                                                                                                                                                                                  A; Accession: S62610
A; Molecule type: protein
A; Residues: 77-99 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: GDB:TNF; TNFA
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Search completed: June 22, 2005, 06:03:12 Job time : 28.813 secs

Biank (uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 22, 2005, 05:57:23 ; Search time 115.832 Seconds (without alignments) 1242.266 Million cell updates/sec Run on:

US-10-662-429-2 1478 Title: Perfect score:

1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched: 1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P50591 homo sapien	Q8k3g0 rattus norv		Q7t1f2 gallus gall			_		Q6jsd9 homo sapien	Q9ese2 r tumor nec	035235 m tumor nec	O14788 h tumor nec	P41047 mus musculu	Q9bdn1 cercocebus	homo sa	P63308 macaca fasc	P63307 macaca mula	-		gall		_		P36940 rattus norv	Q9wv90 marmota mon	Q80yz0 mus musculu	Q8k3y7 rattus norv	Q8nfe9 homo sapien		Q6j3q6 canis famil	095150 homo sapien
SUMMARIES	ID	TN10 HUMAN	Q8K3G0	TN10 MOUSE	Q7T1F2	Q6DHG9	6XXZLO	Q90WT9	Q9DDZ5	Q6JSD9	TN11_RAT	TN11 MOUSE	TN11_HUMAN	TNF6_MOUSE	TNF6_CERTO	TNF6_HUMAN	TNF6_MACFA	TNF6_MACMU	TNF6_MACNE	Q7MTV9	TNF5_CHICK	TNF6_PIG	QBK3Y8	Q861W5	TNF6_RAT	06VW6Q	QBOYZO	Q8K3Y7	Q8NFE9	TNFS_BOVIN	Q6J3Q6	TN15_HUMAN
	DB	-	N	Н	~	7	~	~	~	~	-	-	ч	-	Н		~	-	-	~	-	-	~	~	П	N	N	~	~	Н	N	7
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. de	Query Match	100.0	65.2	62.9	54.8	39.1	22.6	20.8	20.7	19.7	18.1	17.5	17.0	12.8	12.7	12.6	12.5	12.5	12.5	12.5	12.4	12.3	12.2	12.1	12.0	11.9	11.8	11.7	11.2	11.1	11.1	10.8
	Score	14.78	963	930	809.5	577.5	334.5	307.5	305.5	291	267.5	258.5	251.5	189.5	187	186	185	185	185	184.5	184	182	m	178.5	177.5	175.5	175	173	166	164	163.5	160
	Result No.		7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18		20	21	22	23	24	22	56	27	28	53	30	31

043557 homo sapien Q8mj19 macaca mula Q7t2q3 cyprinus ca Q9qyh9 mus musculu Q9bdn3 callithrix Q9bdn3 actus trivi Q97605 fells silve Q6u817 lateolabrax P63304 macaca mula Q97626 canis famil P29965 homo sapien Q70332 mesocricetu Q95mg5 sus scrofa
TN14 HUMAN QBMJ19 Q77203 TN14 MOUSE TNF5 CALJA TNF5 ACTTR TNF5 PELCA QGUB17 TNF5 CERTO TNF5 CERTO TNF5 CANFA TNF5 HUMAN O70332 TNF5 PIGA
-00
240 1240 2224 261 261 261 261 261 261
00000000000000000000000000000000000000
159.5 153.5 153.5 153.5 160.5 149.5 148 147.5 144.5
00000000000000000000000000000000000000

ALIGNMENTS

RESULT 1

X-RAY

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GO; GO:0016020; C:membrane; IEA.
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Submitted (MAY-2002) to the
EMBL, AY115578; AAM49797.1;
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                         X-XX CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
Sung Y.C., Oh B.-H.;
"2.8 A resolution crystal structure of human TRAIL, a cytokine with
selective antitumor activity.";
Immunity 11:253-261(1999).
IFFORTION: Cytokine that binds to TNFRSF10A/TRAILR1,
TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10B/TRAILR4 and
possibly also to TNFRSF11B/OFG. Induces apoptosis. Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OFG that cannot
induce another and TNFRSF11B/OFG that cannot
                                                                            MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5; Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.; "Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5."; Mol. Cell 4:563-571(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  per
                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.

PubMed=10542098; DOI=10.1038/14935;

Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,

Jones E.Y., Screaton G.Y., Chen N., The Control of the TRALL-DRS complex reveals mechanisms conferring specificity in apoptotic initiation.";

Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induce apoptosis. COFACTOR: Binds 1 zinc ion and one anionic solvent molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:000517; P:receptor binding; TAS.
GO; GO:0007267; P:receptor binding; TAS.
GO; GO:0007267; P:induction of apoptosis; TAS.
GO; GO:00043123; P:positive regulation of I-kappaB kinase/NF-k.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006993; TNF family.
InterPro; IPR008993; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and prostate. SIMILARITY: Belongs to the tumor necrosis factor family.
               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                             CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR EMBL, BC032722, AAH32722.1; -.
DR PDB; 1D0G; X-ray; A/B/D=114-281.
R PDB; 1D20, X-ray; A=114-281.
R PDB; 1D4V; X-ray; B=119-281.
R PDB; 1D4V; X-ray; B=119-281.
R PDB; 1D4V; X-ray; D/B/F/J/K/L=114-281.
R PDB; 1D03; X-ray; D/B/F/J/K/L=114-281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U37518; AAC50332.1; -. EMBL; U57059; AAB01233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
mouse cDNA sequences.";
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
PROSITE; PS50049; TNF 2; 1.
3D-structure; Apoptosīs; Cytokine; Metal-binding; Signal-anchor;
Transmembrane; Zinc.
                                                                                                           Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1478; DB 1; Length 281; 100.0%; Pred. No. 4.4e-113; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32509 MW; DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 AA
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52 52 N
291 AA; 33477 MW;
                                                                                                                                                                    EMBL; U37522; AAC52345.1; -. HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 65.6%;
Matches 177; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=TRAIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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Q7T1F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 HITGITRESNLALIPISKDGKTLGQKIETWESSRRGHSFLMHVHLRNGELVIQEGGLYYI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSQTYFRFQE--EIKENTKND----KQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that induces apoptosis.";
Immunity 3:673-682(1995).
-- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
-- FUNCTION: TRANST10B/TRAILR2, TNFRSF10B/TRAILR3, TNFRSF10B/TRAILR4 and
possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.,
"Identification and characterization of a new member of the TNF family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPSLGQ----TCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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-!- TISSUE SPECIPICITY: Widespread.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
      GO:0005164; F:tumor necrosis factor receptor binding; IEA
                                                                                                                                                                                                                                                                                                                                                                    65.2%; Score 963; DB 2; Length 287;
llarity 67.7%; Pred. No. 8.5e-71;
Conservative 29; Mismatches 51; Indels 1
                                                                                                                       InterPro; IPR003636; TNF_eubf.
Promo; PR00229; TNF; 1.
Promo; PR002012; TNF; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1.
PROSITE; PS0049; TNF_2; 1. UNRNOWN 1.
SROUTE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277
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GO; GO: 0005164; F: tumor .net.c...
GO; GO: 0006555; P: tumune response; IEA.
InterPro; IPRO06052; TNP family.
InterPro; IPRO08983; TNP like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TN10 MOUSE
P50592;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLOVKROLYOLIEEVTLRTFQDTISTVPEKQLSTPPLPRGGRPQKVAAHITGITRRSNSA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 CWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGPYYIYSQTYFRFQEE- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFEL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 VLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
"Molecular Cloning and Characterization of Chicken Tumor Necrosis
Factor (TNP)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
Inducing Ligand (TRAIL).";
J. Vet. Med. Sci. 66:43-650(2004).
EMBL; AB114678; BAC79267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
N-linked (GloNAc. . ) (Potential).
3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor related apoptosis inducing ligand.
                                                                                                                                                                                                                                                      MCD; MCI:107414; Tnfsf10.

MCD; MCI:107414; Tnfsf10.

InterPro; IPR006052; TNF family.

InterPro; IPR003636; TNF Thfs.

InterPro; IPR003636; TNF Subf.

ProDom; PD002029; TNF; 1.

SWART; SM00207; TNF; 1.

PROSITE; PS00021; TNF 1; 1.

PROSITE; PS00021; TNF 1; 1.

PROSITE; PS00049; TNF 2; 1.

Apoptosis; Cytokine; Šignal-anchor; Transmembrane.

DOMAIN

1 7 Cytoplasmic (Potential).

TRANSMEM 18 38 Signal-anchor for type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.9%; Score 930; DB 1; 65.6%; Pred. No. 4.4e-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 KKNDRIFVSVTNEHLMDLDQEASFFGAFLI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
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PRT;
                                                                                                                                                                                                                                                      subf; 1.
                                                                                                                                                                                                                                     Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf; SMART; SM0207; TNF; 1.
PROSITE; PS00205; TNF; 1; 1.
PROSITE; PS50049; TNP_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                             cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
 Jones S.J., Marra M.A.;
                                                                      SEQUENCE FROM N.A. TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tnfsf101 protein.
Name=tnfsf101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                            and mouse
                                                                                                                                                                                                                                                                                                                SEQUENCE
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Q7ZYX9
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MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MA Klausberg R.D., Felingold B.A., Grouse L.H., Derge J.G.,
MA Lausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Richards S.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rizywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                   65 NLDVVESKDRVADPCWQVKWHLGKLIKKMMSRILQENMSAINGDRTQALSR--RDEPPQG 122
                                                                                                                                                                                                                                                                                                                                 68 N-----DEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQ-EKQQNISPLVRERGPQ- 120
                                                                                                                                                                                                                                                                                                                                                                                           ---RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 177
                                                                                                                                                                                                                                                                                                                                                                                                              178 EKGFYYIYSQTYFRFQEE-----IKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCW 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                        8 GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP 67
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                          19;
          GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000516; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
INTERPRO; IPRO06052; TNF family.
INTERPRO; IPRO0363; TNF like.
INTERPRO; IPRO0363; TNF subf.
ProDom; PRO0229; TNF 1.
ProDom; PRO0229; TNF 1.
ProSON; SMO201; TNF subf; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS00251; TNF 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKAEYGLYSVYQGGVFQLKREDRIFVSVSNSDIVDMDKEASFFGAFMI 290
                                                                                                                                                                                                           Query Match 54.8%; Score 809.5; DB 2; Length 304; Best Local Similarity 55.4%; Pred. No. 3.6e-58; Matches 160; Conservative 45; Mismatches 65; Indels 19
                                                                                                                                                                             34658 MW; DFC128B517747C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                               304 AA;
HSSP; P50591; 1D20
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                                                                                                                                                                                SEQUENCE
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Обридэ;
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128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 YFR---FQEEIKENTKND------KQMVQYIY-KYTSYPDFILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 LLLLAAILLQTIAVAVTFIYFSNVLSTWKETFSKSSVSCLMRANLRTIKGQELNGAEGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 SPCWQVKWQLRQLVRK-MILRISEETISTVQEKQQNISPLV----RERGPQRVAAHITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED---DSYWDPNDEESMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AB; TISSUE-Whole body;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 299;
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                                                                                                                                                                                                                             252 DSEYGLYSIYQAGLFQLGSGDRVFVTVSNVSTIDMDEKSSFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 AA; 33526 MW; BA776793D2F11ED5 CRC64;
                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
39.1%; Score 577.5; DB 2;
Best Local Similarity 42.2%; Pred. No. 3.9e-39;
Matches 121; Conservative 57; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA
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                Bridgham J.T., Johnson A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
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                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50049; TNF
SEQUENCE 287 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 IHEKGEYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 LFGEPCMKLAEGIKAYISKVTDSIISKQTLHAARTRTHSYNTTGSKFMTTV------MQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVAAHITGTRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSYMDPND-EE 71
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodesgren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strain-Baril 11350E=Winle Dody;
Strain-Baril 11350E=Winle Dody;
Strain-Baril 11350E=Winle Dody;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BCO44336, JA AA444336.1;
R HSSP; P50591; 1D20.
R ZFIN; ZDB-GENE-010801-1; tnfsf101.
R GO; GO:0006020; C:membrane; IEA.
GO; GO:0006164; F:tumor necrooms factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
R InterPro; IPR009693; TNF_like.
R InterPro; IPR0036983; TNF_like.
R InterPro; IPR003636; TNF_ubf.
R ProDom; PD002201; TNF = ubf; 1.
R SWART; SW00207; TNF_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.6%; Score 334.5; DB 2; Length 317; 29.2%; Pred. No. 3.7e-19; ive 55; Mismatches 113; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AA; 35465 MW; 68F76BC1A40DCB9F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TNF_related apoptosis inducing ligand-like protein.
                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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tes 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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Matches
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120 QRVAAHI-----TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLR 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 PNDEESM-NSPCWQVKWQLRQLVRKMILRTSEETI--STVQEKQQ---NISP-LVRERGP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 SNLEELISNQSC----LKLANTIKAYVATVTENVISRSVVNEAQKSYFNISEGQVATKTL 123
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A Bobe J. Goetz F.W.;

Bobe J. Goetz F.W.;

Toldands in the fish ovary.";

L Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).

R EMBL, AFS20041; AAG47640.1;

R ESFN; ZDB-GENE-010801-1; tnfsf101.

R ZFIN; ZDB-GENE-010801-1; tnfsf101.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

R InterPro; IPR00655; P:memune response; IEA.

R InterPro; IPR00856; INF_subf.

R Pfam; PF00229; INF_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:00516; F:tumor necrosis factor receptor binding; IEA.
GO; GO:00055; P:tumor response; IEA.
Pfam; PF00229; TNF; Immune response; IEA.
PRINTS; PR01234; TNECROSISFCT.
Probom; PD002012; TNF subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.8%; Score 307.5; DB 2; Length 32.3%; Pred. No. 5.3e-17; ive 46; Mismatches 110; Indels
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057941; AAL23702.1; -.
HSSP; PS0591; 1D2Q.
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SMART; SM0207; TNR; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;
                                                                                                                                                                                                                                                                                                                                                           150049; TNF 2; 1.
287 AA; 32092 MW; DB06E1C95087B108 CRC64;
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                                                                                                                                                          120 QRVAAHITGTRGRSNT----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 174
                                                                                                                                                                                                                                                                                                                           106 RVPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQLLKGVGTKCWAP 165
                                                                                                                                                                                                                      47 ORPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTW-ANKSFGAHLYNMTLTNGRL 105
                                                                                                                                                                                                                                                                                          175 VIHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSEE2; Q91Z19;
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 44, Last sequence update)
59-FBB-2003 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator franchear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OSteoclast differentiation factor) (ODF).
Name=Thisfil; SynonymesOpgl, Rankl, Trance;
                                                                                       Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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TISSUR-TIDEAL Done,
MEDLINE-20540945, PubWed=11092398;
Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                       7;
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TISSUE-Lung carcinoma;
Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWOVKWOLKOLVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK
                              Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine tumor necrosis factor ligand superfamily member 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 DAEYALHSVYQGGLFELRAGDEVFVSVSSPTWVYGEDSSSYFGAF 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%; Score 291; DB 2; Length 63; 100.0%; Pred. No. 1.7e-16; ive 0; Mismatches 0; Indels
                                                                                   59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kere J.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;
                              DB 2;
                       ch 20.7%; Score 305.5; DB 2
1 Similarity 37.6%; Pred. No. 5.3e-17;
62; Conservative 37; Mismatches 59
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Name=TNFSF10;
Homo Bapiens (Human).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                      "Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNRSF11 (TRANCE, RANKL, ODF, OPGL) gene.";

Int. J. Dev. Biol. 45:853-859(2001).

Int. J. Dev. Biol. As a second to the second to the rate of the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACF----LKED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          member 11, membrane form.
Tumor necrosis factor ligand superfamily member 11, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor necrosis factor ligand superfamily
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    similarity).
    TISSUS SPECIFICITY: Highly expressed in thymus and bone tissues.
    PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
    SIMILARITY: Belongs to the tumor necrosis factor family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SÜBUNIT: HOmotrimer (By similarity). SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                        C., Mason-Savas A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine, Differentiation; Glycoprotein; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
Signal-anchor for type II membrane
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"Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186 (2000).
                                                                                                                                                                                                MEDLINE=21662371; PubMed=11804028;
Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-St
Safadi F.R., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
Marks S.C. Jr.;
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Extracellular (Potential).
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35370 MW; 4B87A4D706AD098F CRC64;
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N-linked (GlCNAC. .) (Po
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InterPro; IPR00893; TNF like.
InterPro; IPR00836; TNF like.
ProDom; PD00201; TNF; 1.
ProDom; PD002012; TNF; 1.
PROSITE; PS00201; TNF; 1.
PROSITE; PS00201; TNF 1.
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                                                                                                                                   266-318 FROM N.A.
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620784; Infefil.
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318 AA;
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SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPI 220
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                                                                                                                                                 R---VAAHITGT-----RGRS-----NTLSSPNSKNEKALGRKINSWESSRSGH 161
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O35235; O35306; Q9JJK8; Q9JJK9; Q9RIY0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Gateoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
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"TRANGE is a novel ligand of the tumor necrosis factor receptor family
that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                           221 LLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
   - DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hybridoma;
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
MODG B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
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MEDLINE-98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Heu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Tnfsf11; Synonyms=OPGL, RANKL, Trance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
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Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.; "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
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TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
but not in nonlymphoid tispussed in T
cells but not in B cells. A high level expression is also seen in
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-i- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.
-i- DISEASE: Deficiency in Thfsfil results in failure to form lobulo-
                                                                                                                                           MEDLINE=99214075, PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6; Kodalara K., Kodalara K., Kodalara K., Mizuno A., Yasuda H., Shima N., Murakami A., Udda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                          nuclear
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MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
Lum L., Wong B.R., Josien R., Bechera J.D., Erdjument-Bromage H.,
Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
"Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
converting enzyme-like processe in shedding of TRANCE, a TNF family
member involved in osteoclastogenesis and dendritic cell survival.",
J. Biol. Chem. 274:13613-13618(1999).
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Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
"Crystal structure of the TRANCE/RANKI cytokine reveals determinants
of receptor-ligand specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200; Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.; "Crystal structure of the extracellular domain of mouse RANK ligand
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDDLINE-21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of nucle factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
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                                                                       Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=035235-2; Sequence=VSP_006449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                Endocrinology 142:1419-1426(2001).
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                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                    differentiation factor.";
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                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick, irregular growth plates and a relative increase in hypertrophic chondrocytes. SIMILARITY: Belongs to the tumor necrosis factor family.
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Tumor necrosis factor ligand superfamily member 11, soluble form.
                                                                                                                                                                                                                                                                                                                                                EMBL; AF013170; AAC71061.1; -

R EMBL; AF013170; AAC71061.1; -

R EMBL; AF013048; AAB86812.1; -

R EMBL; AB008426; BAA25425.1; -

R EMBL; AB002039; BAA36970.1; -

R EMBL; AB022039; BAA36970.1; JOINED.

R EMBL; AB022037; BAA36970.1; JOINED.

R EMBL; AB022037; BAA36970.1; JOINED.

R EMBL; AB022771; BAA3725.1; -

R EMBL; AB03772; BAA36970.1; JOINED.

R EMBL; AB03772; BAA36970.1; JOINED.

R EMBL; AB003772; BAA36970.1; JOINED.

R EMBL; AB005798; BAA97259.1; -

R EMBL; AB006798; BAA97259.1; -

R EMBL; AB006519; F:protein binding; IPI.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:00042804; F:protein binding; IPP.

GO; GO:00042804; F:protein binding; IPP.

GO; GO:00042804; F:protein binding; IPP.

GO; GO:0005515; P:protein binding; IPP.

GO; GO:000551; PR006052; TPF family.

InterPro; IPR008983; TNF_like.

R Probom; PD00207; TNF; 1.

R SMART; SMO0207; TNF; 1.

R SMART; SMO0207; TNF; 1.
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Signal-anchor for type II membrane
protein (Potential).
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N-linked (GlcNAc. . ) (Potential)
Missing (in isoform 3).
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G -> D (in Ref. 2).
Missing (in Ref. 5)
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PROSITE; PS50049; TNF 2; 1.
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014768; 014723; 096017; 099203;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
06-UUL-2004 (Rel. 44, Last annotation update)
1 unor nerosais factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 -----VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS
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Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEBISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2] SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM D.A. (1905) SUBJECTOR (1908) SECONDER (1908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; Cell 93:165-176(1998).
                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

TISSUE=Bone marrow, and Peripheral blood;

MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;

Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.;
      Length 316;
                                                                                                                                                                                                                                                    10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACF
                                                                                                                                   Indels
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"Determination of human RAWIL isoforms.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
17.5%; Score 258.5; DB 1; 26.4%; Pred. No. 6.3e-13; trive 54; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
Ikeda T., Kuroyama H., Hirokawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ODF)
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TISSUE=Thymocytes;
                                                                     Local Similarity 26.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentiation factor)
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                                                                                  "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=014788-3; Sequence=VSP_006446;
TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in spleen, peripheral blood Leukocytes, bone marrow, heart, placenta, skeletal muscle, stomach and thyroid.
INDUCTION: Up-regulated by T cell receptor stimulation.
PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing (By similarity). The cleavage may be
                                                                                                                                                                                                                                Nagai M., Kyakumoto S., Sato N.;

"Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation."

Biochem. Biophys. Res. Commun. 269:532-536(2000).

-! FUNCTION. Cytokine that binds to TNRRSFIIB/OPG and to TNRRSFIIA/ANK. OSteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
SUBCELULIAR LOCATION: Type II membrane protein (isoforms 1 and 3), secreted (isoform 2). A soluble form of isoform 1 arises by proteolytic processing (By similarity).
ALTERNATIVE PRODUCTS:
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190; Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                          TISSUE=Tongue;
MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:005576; C:extracellular; NAS.
GO; GO:005887; C:integral to plasma membrane; NAS.
GO; GO:005887; C:integral to plasma membrane; NAS.
GO; GO:000516; P:tumon necrosis factor receptor binding; NAS.
GO; GO:0030316; P:immune response; NAS.
InterPro; IPR006052; THE family.
InterPro; IPR008983; THF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalyzed by ADAM17.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=SODF;
IsoId=014788-2; Sequence=VSP_006447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=O14788-1; Sequence=Displayed;
                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF019047; AAB86811.1; -. EMBL; AF053712; AAC39731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB064269; BAB79694.1; -
EMBL, AB061227; BAB71768.1; -
EMBL, AB064270; BAB79695.1; -
EMBL, AF013717; AAC51762.1; -
FWRL: AB037599; BAA80488.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF013171; AAC51762.1;
EMBL; AB037599; BAA90488.1;
HSSP; O35235; 1JTZ.
Genew; HGNC:11926; TNFSF11.
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160 LEAQPF-----AHLT----INATDIPSGSHKVSL---SSWYHDR-GWAKISNM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 TFSNGKLIVNODGFYYLYANICFRHHETSGDLATEYLQLMYYYKTKISIKIPSSHTLMKGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 -DSYWDPNDEESMNSPCWQVKW------QLRQLVRKMILRTSEETI-----STVQEKQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                      member 11, membrane form.

Tumor necrosis factor ligand superfamily member 11, soluble form (By similarity).

Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).

Extracellular (Potential).

N-linked (GLNAc. .) (Potential).

N-linked (GLNAc. .) (Potential).

Missing (In isoform 3).

/FIIdavSp 006446.
                                                                                                                                                                                                                                                                                                                                                                                                                                              42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF
                                                                                                                                                                                                                                                                                                                                                                                                                           10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED---
                                                                            Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                            45; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM FASL).
MEDILINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;
Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
Suda T., Nagata S.;
"Generalized Lymphoproliferative disease in mice, caused by a point
multation in the Pass ilgand.";
cell 76:969-976(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
           PROSITE; PS00251; TNF_1; FALSE_NBG.
PROSITE; PS50049; TNF_2; 1.
Alternative splicing; Cytokine; Differentiation; Glycoprotein;
Receptor; Signal-anchor; Transmembrane.
CHAIN

Tumor necrosis factor ligand supe:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (PAS antigen
                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 251.5; DB 1; Length 317; 24.1%; Pred. No. 2.4e-12; tive 61; Mismatches 117; Indels 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                             /FIId=VSP 006447.
A -> G (in Ref. 4).
766176446348097F CRC64;
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                               35478 MW;
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Best Local Similarity 24....
Best Local Similarity 24....
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P41047; Q61217; Q9R1F2;
SM00207; TNF; 1.
                                                                                                          317
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171
198
47
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68
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                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                      DOMAIN
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SMART;
                                                                                                                                         DOMAIN
                                                                                                          CHAIN
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STRAIN=BALB/C;
                     Proc. Natl.
                    ragita H.
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non-profit institutions as long MGD, MGT:99255; Thiesf6.
InterPro; IPR008064; Fas ligand.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
Pfam; PF00229; TNF; 1. 261 TNEHLIDMDHEASFFGAF 278 SEO SOLSLINFEESKTFFGLY 277 EMBL; AF119335; AAB52106.1; -. PIR; A53062; A53062. 279 AA; 31442 MW; U10984; AAA19778.1; -. S76752; AAB33780.1; -. U58995; AAB02915.1; -. EMBL; U06948; AAA17800.1; -. Local Similarity 25.8 es 51; Conservative 218 218 273 184 101 DISULFID CARBOHYD SEQUENCE Query Match *TRANSMEM* CARBOHYD VARSPLIC VARIANT VARIANT VARIANT DOMAIN DOMAIN DOMAIN EMBL; EMBL; 셤 유 셤 ઠે ò ò This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its FUNCTION: Cytokine that binds to TWFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TWFRSF6/FAS-mediated apoptosis and in T cell development. TWFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TWFRSF6B/DCR3 modulates its effects (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
Secreted (isoforms FASL and FASLS). [3]
SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7513(94)90106-6;
MEDLINE=95196085. M.L., Alderson M.R., Baum P.R., Miller R.E.,
Lynch D.H., Watson M., Davis-Smith T., Smith C.A., Hunter K.;
Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
"The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF Isold=P41047-2; Sequence-VSP 006445; PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

DISEASE: A deficiency in protein is the cause of generalized lymphoproliferation disease phenotype (gld). Gld mice present lymphadenopathy and autoantibody production. The phenotype is Fenner M.H., Shioda T., Isselbacher K.J.; "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two MEDLINE-97268671; PubMed-9108079; DOI=10.1073/pnas.94.8.3914; Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K., Peitsch M.J., Tschopp J.J.; "Comparative molecular modelling of the Fas-ligand and other members MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8; STRAIN=C3H; TISSUE=Spleen;
MEDLINE=20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand; a new alternatively spliced product of the mouse Fas ligand gene."; VARIANTS ALA-184 AND GLY-218. STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and MEDLINE=96091792; PubMed=7495745; Adhroeter M., Lowin B., Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B., Rousseau M., Bron C., Renno T., French L., Tschopp J.; "Characterization of the non-functional Fas ligand of gld mice."; 'Polymorphism of murine Fas ligand that affects the biological recessively inherited. SIMILARITY: Belongs to the tumor necrosis factor family. Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases Event=Alternative splicing; Named isoforms=2; IsoId=P41047-1; Sequence=Displayed; SEQUENCE FROM N.A. (ISOFORM FASL) (ISOFORM FASLS) CHARACTERIZATION OF VARIANT GLD. Mol. Immunol. 32:761-772(1995). . Immunol. 7:1381-1386(1995) Blood 94:3456-3467(1999). ALTERNATIVE PRODUCTS family."; SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked (GlcNAc. . .) (Potential).
Missing (in isoform FasLS).
/FTId=VSP_006445.
T -> A (in gtrain BALB/c, strain DBA/l and strain DBA/2; enhances cytotoxicity).
E -> G (in strain BALB/c, strain DBA/l and strain DBA/2; enhances cytotoxicity).
F -> L (in gld; abolishes binding of FASL to its receptor).
WW; 37972E272BEDALCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO123; TNF; 1.

PRINTS; PRO1261; PASLIGAND.

PRINTS; PRO1261; TNECROSISFCT.

PRODOM; PD002012; TNF subf; 1.

PROSITE; PS50049; TNF 2; 1.

PROSITE; PS50049; TNF 2; 1.

Alternative splicing; Apoptosis; Cytokine; Disease mutation;

Alternative splicing; Apoptosis; Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 ELREFTNOSL-----KVSSFEKQIANPSTPSEKKEPRSV-AHLTG------NPHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor necrosis factor ligand superfamily member 6, soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Indels
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Poly-Pro.
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TISSUE=Leukocyte;
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CARBOHYD
CARBOHYD
CARBOHYD
                                           SEQUENCE
                                                                      Query Match
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TISSUELLymphocytes;

MEDILNE-21983618; PubMed=11491535; DOI=10.1007/8002510100322;

MEDILNE-21983618; PubMed=11491535; DOI=10.1007/8002510100322;

Willinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,

Weiss W.R., Ansari A.A.;

Toloning, sequencing, and homology analysis of nonhuman primate

Transpace in and co-estimulatory molecules.";

Test/Fas/Fas-ligand and co-estimulatory molecules.";

Temunogenetics 53:315-328(2001).

Tennomic Cytokine that binds to TNFRSF6/FAS, a receptor that

Transduces the apoptotic signal into cells. May be involved in

Cytotoxic T cell mediated apoptosis and in T cell development.

TNFRSF6/FAS-mediated apoptosis may have a role in the induction of

Deripheral tolerance, in the antigen-stimulated suicide of mature

To cells, or both. Binding to the decoy receptor TNFRSF6/DCR3

modulates its effects (By similarity).

Collected (By similarity).

Collected (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYODOW, ...
SMART, SM0207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
Tumor necrosis factor ligand superfamily member 6, membrane form.
member 6, membrane form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor necrosis factor ligand superfamil
member 6, soluble form (By similarity).
Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                    Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolytic processing (By similarity). SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (Potential).
Extracellular (Potential)
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Potential.
                           280 AA
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                                                                                                           (CD95L protein).
Name=TNFSF6; Synonyms=CD95L, FASL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008064; Fas ligand.
InterPro; IPR006053; TNF-abc.
InterPro; IPR006053; TNF-abc.
InterPro; IPR008093; TNF-like.
InterPro; IPR008093; TNF-like.
InterPro; IPR003636; TNF-subf.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNCROSISFCT.
ProDom; PD002012; TNF subf; 1.
SWART; SM0207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF344847; AAK37606.1; -.
HSSP; P50591; 1D2Q.
                                                        (Rel. 41, Created)
                                                                                                                                                                               Cercopithecinae; Cercocebus.
                           STANDARD;
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101
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69
64
129
232
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128
201
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28-FEB-2003 (
05-JUL-2004 (
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DOMAIN
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DISULFID
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                                     Q9BDN1;
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118
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                                                                                                                                                                                                                                                                                                                                                                        64 YWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVA 123
                                                                                                                                                                                                                                                                                                                                                                                                                            119 -------PREVEGERY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 183
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                                                                                                                                                                                                                                                                                         4 MEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 IYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNSCWSKDAEYGLYSI
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Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
"Human Fas ligand: gene structure, chromosomal location and species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-95071350; PubMed=7980502;
MICLA E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
Fusamoto H., Kamada T.,
"Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                                                                                                                                                    68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Fas ligand mediates activation-induced cell death in human
                                                                                                                                         12.7%; Score 187; DB 1; Length 280; 22.1%; Pred. No. 4e-07;
                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOPORM 1).
Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
183 N-linked (GlCNAC. . .) (Pc
249 N-linked (GlCNAC. . .) (Pc
259 N-linked (GlCNAC. . .) (Pc
31407 MW; 729EA60067B7D398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 YLGAVFNLTSTDHLYVNVSELSLVNFEESQTFFGLY 278
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                                                                                                                                                                    Pred. No. 4e-07
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 AA
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MEDLINE=95105731; Pubmed=7528780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            int. Immunol. 6:1567-1574(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exp. Med. 181:71-77(1995).
                                                                                                                                                                      22.1%;
                                                                                                                                                                 Local Similarity 22.1 les 61, Conservative
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183
249
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183
249
259
280 AA;
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DOMAIN
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  **REDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
**Altasner R.D., Collins F.S., Wagner L., Sheafer C.F., Bhat N.K.,
**Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
**Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
**Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
**Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
**Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
**Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
**Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
**An S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
**An S. Morley K.C., Hale S., Garchen A.M., Gay L.J., Hulyk S.W.,
**An S. Malan A., Young A.C., Shevchenko Y., Bouffard G.G.,
**Mhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,
**Butterfield Y. S. M., Krzywinski M.I., Skalaka U., Smallus D.B.,
**Butterfield X. Schmin J.B., Worsen M.A.,
**Schein J.B., Wong A.C., Grimwood J., Schmutz J., Myers R.M.,
**Schein J.B., Wong A.C., Grimwood J., Schmutz J., Marra M.A.,
**Schein J.B., Wong A.C., Grimwood J., Schmutz J., Skalaka U., Smallus D.B.,
**Schein J.B., Wong A.C., Grimwood J., Schmutz J., Marra M.A.,
**Schein J.B., Wong A.C., Grimwood J., Schmutz J., Skalaka J., Smallus D.B.,
**An Butterfield Y. S. N., Krzzywinski M.I., Skalaka J., Smallus D.B.,
**An Bond J., Schmutz J., Swalaka J., Smallus D.B.,
**An Bond J., Schmutz J., Swalaka J., Smallus D.B.,
**An Bond J., Schmutz J., Swalaka J., Smallus D.B.,
**An Bond J., Schmutz J., Swalaka J., Sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeytun A., Nagarkatti M., Nagarkatti P.S.;
"Isolation and characterization of a new naturally occuring variant of human Fas ligand that is expressed only in membrane bound form."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolytic processing.
DISBASE: Defects in TNRSF6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275. MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827; Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P., Terskikh A., Peitsch M.C., Tschopp J.; Terskikh A., Peitsch M.C., Tschopp J.; Characterization of Fas (Apo-1, CD95)-Fas ligand interaction."; J. Biol. Chem. 272:18827-18833 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: N-glycosylated.
PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P48023-1; Sequence=Displayed;
                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS:
                                                                                        [6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Blood;
                                                                                                                                                                                                                            TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1;
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                                                                                                                                    Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@ment(See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0005102; P:cell-cell signaling; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0003123; P:positive regulation of I-kappaB kinase/NF-k. . ; IEP.
GO; GO:0003165; P:signal transduction; TAS.
InterPro; IPR008064; Fas ligand.
InterPro; IPR008053; TNF abc.
InterPro; IPR008053; TNF abc.
InterPro; IPR0080593; TNF abc.
InterPro; IPR0080593; TNF abc.
InterPro; IPR0080593; TNF abc.
InterPro; IPR0080595; TNF abc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor necrosis factor ligand superfamily member 6, membrane form.

Tumor necrosis factor ligand superfamily member 6, soluble form.
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Missing (in isoform 2).
FTId=VSP 006448 binding to TNFRSF6 and reduces cytotoxity more than 100-fold.
Y->F,R: Lowers binding to TNFRSF6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
STSQMHTASSL -> ATPVHPLKKRS (in 180form
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F-51: Abolishes binding to TNRFSF6 and cytotoxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1681; FASLIGAND.
PRINTS; PRO1234; TNECROSISFCT.
PRODOM; PRO02121; TNF subf; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;
                                                                                                        WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674 g.htm".
involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and splanomegaly. SIMILARITY: Belongs to the tumor necrosis factor family. DATABASE: NAME-PROW; NOTE-PROW 2:59-69(2001);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
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HSSP, P50591, 1D2Q.
Genew, HGNC:11936; TNFSF6.
H-InvDB; HIX0001337; -.
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Query Match
12.6%; Score 186; DB 1; Length 281;
Best Local Similarity 22.1%; Pred. No. 4.9e-07;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;
                                                                                           61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG 281 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003bs:* geneseqp2003bs:* A_Geneseq_16Dec04:*
1: geneseqp1980s:*
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3: geneseqp2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	uc	Novel cyt	Human Apo	Human apo	Human TL2		Human AGP	Protein a	Human Apo	Human Apo	Human PRO	Amino aci	Human AGP		Human Apo	Human TNF		Human TRA	Human TRA	Human TNF	Human Apo		C neoform	Human TNF		Human Apo
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	Ω	AAW19777	AAW27134	AAW19787	AAW76829	AAW56760	AAW44354	AAY01517	AAY27012	AAY81956	AAB24038	AAB08545	AAB28691	AAB50977	AAB67243	AAE11031	AAB48350	ABB08133	ABG31630	AAU75062	AAM51077	ABP51954	AA019095	AAU79593	ABG73861	ABU10205
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ABU71443 ABG72738 AAO29543	ABU08558 ABR42313 ABG71905 ABP60546 AAE36258	AAO31151 ABO25125 ADB61471 ADC35202	ADD14080 ADD19010 ABW02276 ADE76953	ADK72311 ADK72303 ADK72304 ADK72296
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24 27 28	9 9 H 8 8	8 8 8 8 8 4 8 4 8 4 8 4 8 4 8 4 8 8 8 8	38 39 44 10	4 4 4 4 3 6 4 7

ALIGNMENTS

AAW19777; 22-SEP-1997	
	(first entry)
Novel cytokine	Novel cytokine Apo-2 ligand.
Apo-2 ligand;	Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.
Homo sapiens.	
Key	Location/Qualifiers
Peptide	1281 /note= "Claim 4"
Region	1. 14
Protein	/ tabets cycopiasmic_region
Dogion	/note= "Claim 3"
weg ton	/label= Transmembrane region
Protein	41281 /note= "Claim 2"
Region	41281
Modified-site	/ rabels Extracellular_region 109
	/label= Glycosylation /note= "putative N-linked glycosylation site"
Protein	114281 /note= "Claim 1"
WO9725428-A1.	
17-JUL-1997.	
08-JAN-1997;	97WO-US000272.
09-JAN-1996;	96US-00584031.
(GETH) GENENTECH INC	TECH INC.
Ashkenazi AJ,	Chuntharapai A, Kim KJ;
WPI; 1997-372867/34 N-PSDB: AAT72796.	867/34. 796.

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                                                             A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays
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                                                                                                                                                                                                                                                                                                    MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis inducing molecule-I, AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily, AIM-I altered expression; neoplasia inhibition; anti-inflammatory agent.
NOVEL CYCOKINE, ADO-2 ligand and corresponding DNA - used to induce apoptosis for the treatment of breast and colon cancer.
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                                                                                                                                                                                                                              100.0%; Score 1478; DB 2; Length 281; 100.0%; Pred. No. 3.8e-137; ive 0; Mismatches 0; Indels 0
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                                        4; Fig la; 72pp; English.
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Matches 281; Conservative
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                                         Claim
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WPI; 1997-470807/43. N-PSDB; AAT85210.

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AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand superfamily. The products can be used in the diagnosis and treatment of disorders related to under-expression, over-expression or altered capression of AIM-I. AIM-I or agonists can be used for treating autoimmunoproliferative disease lymphadenopathy (TRL), rheumatosus, immunoproliferative disease lymphadenopathy (TRL), rheumatoid arthritis, diabetes, and multiple sclenosis, graft versus host disease, to inhibit neoplasis auch as tumour cell growth, to treat restenosis, to requlate neoplasis in endothelial cell development, to stimulate peripheral colerance and cytocoxic T-cell mediated apoptosis. Antagonists can be used for treating cachexia, cerebral malaria, rheumatoid arthritis or osteoporosis, for preventing graft-host rejection, and as anti-inflammatory agents, for treating endotoxic shock or to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
New isolated apoptosis inducing molecule-I - used to develop products for the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft versus host disease or inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                               sequence represents a human Apoptosis inducing molecule-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1478; DB 2;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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/label= Transmembrane_domain
39. .281
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/label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human apoptosis inducer cytokine TRAIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW19787 standard; protein; 281
                                                                                                  Claim 2; Fig 1; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 100.
281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
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AAW19787
ID AAW1
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inflammation, arthritis, septicaemia, autoimmune disease, restenosis, transplant rejection, infection, ischaemia; brain injury; bone disease; acute respiratory disease syndrome, acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polymucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune disease (e.g. inflammatory bowel disease, isochaemia, autoimmune disease (e.g. inflammatory bowel disease, isochaemia, acute respiratory disease syndrome, restenois, brain injury, (acquired autoimmune disease syndrome, bone disease, cancer (e.g. lympho-proliferative disease), atherosclerosis and Alzheimere disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DDSYMDPNDEESMNSPCWQVXWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                             tumour necrosis factor related receptor; human; treatment; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1478; DB 2; 100.0%; Pred. No. 3.8e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding tumour necrosis factor receptor TR6 polypeptide, antibody, agonist, antagonist, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 32-33; 34pp; English.
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97US-00853684.
97US-00916625.
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N-PSDB; AAV63096.
                          (first
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Best Local Similarity
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                                                                   Human TL2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 281 AA;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-1997;
09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
                          25-JAN-1999
                                                                                                                                                                                                                                                                                                                                             14-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAM19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine, induces apoptosis in cancer and virus-infected for treating thrombotic microangiopathy, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                   site"
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/label= Extracelular domain
/note= "contains a receptor-binding region"
                                         89. .90
/note= "potential KEX2 protease processing
                                                                              109. .111 /note= "potential N-glycosylation site" /149. .150 /note= "potential KEX2 protease processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 43-44; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIL, a novel cytokine, induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection and for use in assays.
                                                                                                                                                                                                                                                                                                                  95US-00496632.
95US-00548368.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Goodwin RG;
                                                                                                                                                                                                                                                                                                                                                                                  (IMMV) IMMUNEX CORP.
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                                           Cleavage-site
                                                                                 Modified-site
                                                                                                                                                                                        WO9701633-A1
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01-NOV-1995;
                                                                                                                                                                                                                                   16-JAN-1997
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Wiley

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AAW76829 standard; protein; 281

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Length 281; Indels

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The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resobretion. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus or the accorption diseases (e.g. osteoporosis, osteomyelitis, chematopoietic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to
                         181 FYYIYSQTYFRFQEEIKENTKNDKQWVQXIXKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour necrosis factor-related protein; INF; inflammation;
FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                               241 SIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 3.8e-137;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone resorption; haematopoietic disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-042194/04.
N-PSDB; AAV15295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; AGP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9746686-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human AGP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1998
                                                                                                                                                                                                                                                                                                                     AAW44354;
181
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Matches
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                                                                                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This represents a human tumour necrosis factor related apoptosis ligand (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful for producing the recombinant TRAIL polypeptides, which may be useful in studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections.
                                                                                                                                                                                                                                                                      Tumour necrosis factor related apoptosis ligand; TRAIL; research; human; cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-terminal cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1478; DB 2;
100.0%; Pred. No. 3.8e-137;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                        AAW56760 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 33-36; 28pp; English.
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95US-00548368
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39.
                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                     Human TRAIL polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                            .18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1996;
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01-NOV-1995;
                                                                                                                                                                       05-AUG-1998
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                                                                                                                         AAW56760;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes the use a polypeptide corresponding to at disast the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory disease. The polypeptides can be used in treatment of neurodegenerative disease. The polypeptides can rhuematoid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and anti-TRAIL antibody or a TRAIL equivalent that binds to specific at receptors, inhibiting formation of natural complex
                                                           180
                                                                                                                   240
                DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPO 120
                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                    181 FYYIYSQTYFRFQEEIKENTKNDKQWVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                         Neurodegenerative disease; autoimmune disease; inflammatory disease;
lupus erythematosus; rhuematoid arthritis; SEP; apoptotic;
surface receptor; TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                   Protein associated with neurodegenerative and autoimmune diseases.
                                                                                                                                                                         SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                            AAY01517 standard; peptide; 281 AA
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                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-156177/14.
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This sequence represents a novel human cytokine, designated Apo-2 ligand (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant methodology. Apo-2L is useful for inducting apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immunemainted glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases
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61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                            180
                                                              121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                           240
                                                                                                                             191 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human.
                                          121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                           PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                         241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1478; DB 2;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                         Human Apo-2 ligand (Apo-2L) polypeptide.
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                                                                                                                                                                                                                                                                                          AAY27012 standard; protein; 281
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Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kelley
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N-PSDB; AAX86987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1999;
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

100.0%; Score 1478; DB 2; Length 281; 100.0%; Pred. No. 3.8e-137; ive 0; Mismatches 0; Indels 0

Query Match Best Local Similarity 100.º Matches 281, Conservative

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Indels

Score 1478; DB 3;
Pred. No. 3.8e-137;
0; Mismatches 0;

100.0%;

Length 281;

9 60 180

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181 FYYIYSQTYFRFQEEIKENTKNDKQNVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                   RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                      Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated monoclonal antibodies having antigen specificity for Apo-2 ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo -2 ligand serum, and for treating diseases associated with increased
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                                                                                                                   61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                      61 DDSYMDPNDEBSMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGTACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Apo-2 ligand protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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AAY81956

AAY8196

AAY8196
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The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO357; PRO1597; PRO1597; PRO1597; PRO1597; PRO1595; PRO1096; PRO2098; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to
                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression.
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                                                                                                          proliferation; cancer;
                                                                                                                                                                                                                                                                                                                                                                    Wood
                                                                                                                                                                                                                                                                                                                                                                    Watanabe CK,
                                                                                                          Human; tumour; diagnosis; neoplastic disease; prolife: identification; tumourigenesis; anticancer; detection
                                                                                                                                                                                                                                                                                                                                                                     Roy MA,
                                                                                Human PRO1096 protein sequence SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                     Gurney AL,
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AAB24038 standard; protein; 281
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Goddard A,
                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Sequence 281 AA;

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diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AACS8019 to AACS8102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AACS8013 to AACS8122 and AABZ4021 to AABZ4040 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
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                                                                                                                                                                                                                100.0%; Score 1478; DB 3; Length 281; 100.0%; Pred. No. 3.8e-137; ive 0; Mismatches 0; Indels 0;
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Matches 281, Conservative
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The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducting ligand) polymeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                    100.0%; Score 1478; DB 3;
100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
Disclosure; Page 23-24; 29pp; English.
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N-PSDB; AAC67831.
                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                    Sequence 281 AA;
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                                                                                                                                                                                        lung carcinoma)
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                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an Fc immunoglobulin region fused to the Nerminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodaficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins used in prior art therapies
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Pusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
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antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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99US-0140650P.
99US-0141037P.
99US-0144758P.
99WO-US020594.
                                                                                            2; 93pp; English.
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                            3; Fig
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20-JUL-1999;
01-SEP-1999;
08-SEP-1999;
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                                                                                            Claim
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Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and amall molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
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Pred. No. 3.8e-137;
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                                                                                                                                                                                                                                                                                                                          Gurney AL, Hebert C,
Watanabe CK, Wood WI;
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100.0%; Pred. No. s..
0; Mismatches
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                                                                                                                          11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US004342.

02-MAR-2000; 2000WO-US005841.

03-MAR-2000; 2000WO-US00581.

10-MAR-2000; 2000WO-US00681.
                            99WO-US028634.
99WO-US028551.
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17-MAY-2000; 2000WO-US013705.
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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N-PSDB; AAC91579.
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                                                                            16-DEC-1999;
20-DEC-1999;
06-JAN-2000;
             30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
09-DEC-1999;
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AAB67243
ID AAB67
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AAB67243 standard; protein; 281

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The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target calls, including cancer calls and virally infected cells. The TRAIL polypeptides are useful in killing cancer calls, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HTV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
                                Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection; human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
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/label _ N_terminal_cytoplasmic_domain
related apoptosis inducing ligand (TRAIL)
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Pred. No. 3.8e-137;
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/label= Extracellular_domain
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95US-00548368.
96US-00670354.
98US-00048641.
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Best Local Similarity
Matches 281; Conserv
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10-NOV-1998;
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 Human TNF
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                                                                                           melanoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                            divalent metal ions; viral infection; cancer.
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Pai R, Shahrokh Z, Simmons L;
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                                                                                                                                                                                                                                                                         26-JUN-2000; 2000WO-US017579
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Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                          Human; Apo2 ligand:
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O'connell M,
                                                                                                                                                                                                                                                                                                             28-JUN-1999;
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                                                     18-APR-2001
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Search completed: June 22, 2005, 06:07:13 Job time : 128.948 secs

Sequence 5, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli

US-10-218-547-20 US-10-322-673-72 US-10-319-785-66 US-10-310-793-26 US-10-279-687-8 US-10-279-687-8 US-10-279-687-8 US-10-662-429-2 US-10-662-430-2 US-10-662-431-2 US-10-662-431-2 US-10-662-431-2 US-10-662-431-2 US-10-682-284-2 US-10-825-282-24 US-10-861-85-11 US-10-861-85-11 US-10-978-333-11 US-10-978-333-11 US-10-978-333-11 US-10-978-333-11 US-10-978-131-23 US-10-978-131-23 US-10-978-131-23 US-10-978-131-23

Sequence 1, Al Sequence 1, Al Sequence 3, Al Sequence 22, I Sequence 23, I

Sequence 10, Sequence 13, A Sequence 30, Sequence 16, A

ALIGNMENTS

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Sequence 6, Application US/08916625B
; Publication No. US2010010924A1
; GENERAL INFORMATION:
    APPLICANT: DEEN, KEITH C.
    APPLICANT: TOUNG, PETER R.
    TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
    TITLE OF INVENTION: RECEPTOR, TR6
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
    ADDRESSEB: RATNER & PRESTIA
    STREET: P.O. BOX 980
    CITY: VALLEY FORGE
    STATE: PA
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,625B
FILING DATE: 22-AuG-1997
CLASSIFICATION NAMBER: 08/83,684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041,230
APPLICATION NUMBER: 80/041,230
APPLICATION NUMBER: 80/041,230
APPLICATION NUMBER: 23,031
   JS-08-916-625B-6
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   Sequence 6, Appli
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Sequence 17, Appl
Sequence 8, Appli
Sequence 11, Appli
Sequence 118, Appli
Sequence 4, Appli
Sequence 54, Appli
                                                                                                      June 22, 2005, 06:01:21 ; Search time 652.628 Seconds (without alignments) 165.329 Million cell updates/sec
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Sequence 11,
Sequence 41,
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12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-911-317A-8
US-09-813-329-17
US-09-193-663-8
US-09-934-465-1
US-09-919-019-118
US-10-011-125-4
US-10-010-054-54
US-10-0174-654-11
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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TELEFAX: (847) 938-2623
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Publication No. US20010010925A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FREESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REPERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION:
TELEPHONE: (847) 935-7550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                            Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 281; Conservative 0;
                 TELECOMMUNICATION INFORMATION TELEPHONE: 610-407-0700 TELEFAX: 610-407-0701
                                                  TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
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 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                         US-08-916-625B-6
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US-08-971-317A-8
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Sequence 17, Application US/09813329

Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICAMY: Bristol-Myers Suibb Company
ITILE OF INVENTION: Variants Thereof
TILE OF INVENTION: Variants Thereof
TILE REFERENCE: D0016.np
CURRENT PAPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR PAPLICATION NUMBER: 60/190,816
PRIOR PAPLICATION NUMBER: 60/190,816
SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
SEQ ID 077
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100.0%; Pred. No. 1.5e-128;
tive 0; Mismatches 0;
                                                                                                                                                                                                           100.0%; Score 1478; DB 8;
100.0%; Pred. No. 1.5e-128;
tive 0; Mismatches 0;
                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925Ale
US-08-971-317A-8
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ORGANISM: Drosophila melanogaster
INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acids TYPE: amino acid
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Matches 281; Conservative
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                                                                                           STRANDEDNESS: single
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                                                                                                                                                                                              Sequence 8, Application US/09193663

Patent No. US2002055624A1

GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
FILE REPRENCE: 6255.US.02
CURRENT APPLICATION NUMBER: 05/09/193,663

CURRENT FILING DATE: 1998-11-17

SEALLER APPLICATION NUMBER: 60/065,916

EARLIER APPLICATION NUMBER: 60/065,916

SALUER FILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                          241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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; Patent No. US20020102233A1
; GENERAL INFORMATION:
APPLICANT: APARhemazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT PILING DATE: 1996-01-09
; PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PATENTIN Ver: 2.0
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CONGANISM: Homo sapiens
US-09-934-465-1
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 281
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US-09-934-465-1
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Sequence 118, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
TITLE OF INVERTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TITLE OF INVERTION GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
SEQ ID NO 118
LENGTH: 281
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Length 281;
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-139-118
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100.0%; Score 1478; DB 9;
100.0%; Pred. No. 1.5e-128;
iive 0; Mismatches 0;
  Query Match
Best Local Similarity 100.
Matches 281; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Hebert, Carciyn
APPLICANT: Kabakoff, Milliam
APPLICANT: Kabakoff, Milliam
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034R1PCT
FILE REPERENCE: P3034R1PCT
FILE REPERENCE: P3034R1PCT
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PILLING DATE: 1997-09-17
PRIOR PILLING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR PILLING DATE: 1998-03-30
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                                                                                                                                      TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1004R1
CURRENT APPLICATION NUMBER: US/10/011,125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54, Application US/10001054 Publication No. US20020192209A1 GENERAL INFORMATION:
                                                     Sequence 4, Application US/10011125
Publication No. US20020142388A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker, Kevin
Goddard, Audrey
Gurney, Austin
Hebert, Carolyn
Henzel, William
Kabakoff, Rhona
Shelton, David
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4
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US-10-001-054-54
                                -10-011-125-4
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APPLICANT:
APPLICANT:
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R APPLICATION NUMBER: 60/099803
R FILING DATE: 1998-09-10
R PILING DATE: 1998-09-14
R APPLICATION NUMBER: 60/100263
R FILING DATE: 1998-09-14
R APPLICATION NUMBER: 60/100390
R FILING DATE: 1998-09-15
R FILING DATE: 1998-09-18
R FILING DATE: 1998-11-10
R R FILING DATE: 1998-11-10
R APPLICATION NUMBER: 60/100849
R FILING DATE: 1998-11-10
R APPLICATION NUMBER: 60/108849
R APPLICATION NUMBER: 60/112420 R APPLICATION NUMBER: 60/116533 R FILING DATE: 1999-01-20 A PPLICATION NUMBER: 60/123618 R FILING DATE: 1999-03-10 R APPLICATION NUMBER: 60/131294 R APPLICATION NUMBER: 60/140650 R APPLICATION NUMBER: 60/140650 RAPPLICATION NUMBER: 60/141037

R FILING DATE: 1999-66-23

R FILING DATE: 1999-67-20

R APPLICATION NUMBER: 60/14258

R APPLICATION NUMBER: 60/162506

R APPLICATION NUMBER: 60/162506

R FILING DATE: 1999-10-29

R FILING DATE: 1999-10-29

R FILING DATE: 1999-12-09

R FILING DATE: 2000-03-03

R APPLICATION NUMBER: 60/19022

R FILING DATE: 2000-06-05

R APPLICATION NUMBER: 60/209832

R APPLICATION NUMBER: 60/209832 R APPLICATION NUMBER: 09/180997
R FILING DATE: 1998-11-19
R FILING DATE: 1998-12-22
R APPLICATION NUMBER: 09/284291
R APPLICATION NUMBER: 09/284291
R APPLICATION NUMBER: 09/380137
R APPLICATION NUMBER: 09/380137
R FILING DATE: 1999-08-25 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/085149 FILING DATE: 1999-09-09 APPLICATION NUMBER: 09/403297 FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/423741 FILING DATE: 1999-11-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/090691 APPLICATION NUMBER: 60/115554 FILING DATE: 1999-01-12 APPLICATION NUMBER: 60/115558 FILING DATE: 1999-01-12 APPLICATION NUMBER: 09/380138 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380913 APPLICATION NUMBER: 60/113296 FILING DATE: 1998-12-22 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/096891 FILING DATE: 1998-08-17 APPLICATION NUMBER: 60/096894 FILING DATE: 1998-08-17 FILING DATE: 1998-05-12

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R APPLICATION NUMBER: PCT/USO0/04342
R FILING DATE: 2000-02-18
R APPLICATION NUMBER: PCT/USO0/05841
R FILING DATE: 2000-03-02
R APPLICATION NUMBER: PCT/USO0/06884
R FILING DATE: 2000-03-15
R APPLICATION NUMBER: PCT/USO0/08439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-08-28
APPLICATION NUMBER: 09/946374
FILING DATE: 2001-09-04
APPLICATION NUMBER: PCT/US98/18824
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PILING DATE: 1099-12-01
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-09-10
APPLICATION NUMBER: PCT/US99/00106
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APPLICATION NUMBER: PCT/US99/20111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28551
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APPLICATION NUMBER: PCT/US00/00376
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FILING DATE: 2000-02-18
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APPLICATION NUMBER: PCT/US00/13705
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APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US00/15264
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FILING DATE: 2000-08-23
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APPLICATION NUMBER: PCT/US99/28634
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                                                             FILING DATE: 2001-05-25
APPLICATION NUMBER: 09/872035
FILING DATE: 2001-06-01
APPLICATION NUMBER: 09/882636
                              FILING DATE: 2000-11-08
APPLICATION NUMBER: 09/802706
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APPLICATION NUMBER: 09/918585
FILING DATE: 2001-07-30
APPLICATION NUMBER: 09/924419
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APPLICATION NUMBER: 09/927796
FILING DATE: 2001-08-06
APPLICATION NUMBER: 09/929404
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APPLICATION NUMBER: 09/941992
APPLICATION NUMBER: 09/709238
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240 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSBETISTVQBKQQNISPLVRERGPQ 120 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGTACFLKE 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY Gaps Sequence 54, Application US/10093766

Bublication No. US2030013099A1

GENERAL INFORMATION

APPLICANT: Lasek, Amy W.

APPLICANT: Lasek, Amy W.

APPLICANT: Rarpf, Adam R.

TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS

TITLE REPERENCE: PA-0047 US

CURRENT PAPLICATION NUMBER: US/10/093,766

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 61

SEQ ID NO 5: 61 ö 100.0%; Score 1478; DB 13; Length 281; 100.0%; Pred. No. 1.5e-128; ive 0; Mismatches 0; Indels 0; TYPE: PRT
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 PRIOR FILING DATE: 2001-02-28
PRIOR PELICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-39
PRIOR PLING DATE: 2001-06-39
PRIOR PLING DATE: 2001-06-39
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2001-08-29
PRIOR PLING DATE: 2001-08-29 Query Match
Best Local Similarity 100.
Matches 281; Conservative ; TYPE: PRT ; ORGANISM: Homo Sapien US-10-001-054-54 US-10-093-766-54 61 RESULT g 쉽 셤 ઠે ò

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DDSYMDPNDEESMASPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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Publication No. US20030059862A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE APPLICANT: Ruben, Steven M.
TITLE REPRENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
LENGTH: 281
                                                                     1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEETISTVQEKQQN1SPLVRERGPQ
                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                            FYY1YSQTYFRFQEEIKENTKNDKQMVQY1YKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
Indels
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0; Mismatches
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Publication No. US20030100074A1
GENERAL INFORMATION:
281; Conservative
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CRGANISM: Homo sapiens
US-10-151-882-41
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US-10-218-547-20
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US-10-151-882-41
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                                                                                                                                                                                                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                  121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKK
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                                                                                                                                                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPII.LMKSARNSCWSKDAEYGLY
                                                        Gaps
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                 100.0%; Score 1478; DB 14; Length 281; 100.0%; Pred. No. 1.5e-128; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: CUNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 1.5e-128;
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Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-10-174-654-11
Sequence 11, Application US/10174654
Publication No. US20030044937A1
CENERAL INFORMATION:
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LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
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TOPOLOGY: linear
:ULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11:
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COMPUTER READABLE FORM:
                                                      Matches 281; Conservative
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                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                   Gaps
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Query Match
Best Local Similarity 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0;
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61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                                                        1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                       Gaps
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; Publication No. US20030190685A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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  DB 14; Length 281;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Score 1478; DB 14;
100.0%; Pred. No. 1.5e-128;
ive 0; Mismatches 0;
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FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR PLING DATE: 2002-05-07
PRIOR PLING DATE: 2001-05-05
PRIOR FILING DATE: 2001-12-20
PRIOR PLING DATE: 2001-11-3
PRIOR PLING DATE: 2001-11-3
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2001-09
PRIOR PLING DATE: 2001-09
PRIOR PLING DATE: 2001-09
PRIOR PLING DATE: 2001-09
PRIOR FILING DATE: 2001-09-21
PRIOR PLING DATE: 2001-09-21
PRIOR PLING DATE: 2001-09-21
PRIOR PLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 66
LENGTH: 281
Query Match
Best Local Similarity 100.8
Matches 281; Conservative
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Best Local Similarity
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             TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
TITLE OF INVENTION: Human Endokine Alpha
TITLE OF INVENTION: Human Endokine Alpha
TITLE REPERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR APPLICATION NUMBER: 60/310,761
PRIOR PILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-0-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 281
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TITLE OF INVENTION: Receptors
FILE REFERENCE: PF985
CURRENT PILING DATE: 2002-12-19
FRIOR PLING DATE: 2001-12-09
FRIOR PLING DATE: 2001-12-09
FRIOR PLING DATE: 2001-02-04
FRIOR PLING DATE: 2002-04-05
FRIOR APPLICATION NUMBER: 60/369,877
FRIOR PLING DATE: 2002-04-05
FRIOR PLING DATE: 2002-04-05
FRIOR PLING DATE: 2002-04-05
FRIOR PLING DATE: 2002-04-05
FRIOR PLING DATE: 2002-06-04
FRIOR PLING DATE: 2002-06-04
FRIOR PLING DATE: 2002-07-18
FRIOR PLING DATE: 2002-07-18
FRIOR PLING DATE: 2002-07-18
FRIOR PLING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/403,370
FRIOR APPLICATION NUMBER: 60/403,370
FRIOR PLING DATE: 2002-07-18
FRIOR PLING DATE: 2002-07-18
FRIOR PLING DATE: 2002-07-18
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100.0%; Pred. No. 1.5e-128;
iive 0; Mismatches 0;
APPLICANT: Human Genome Sciences, Inc.
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US-10-322-673-72
US-10-322-673-72
is Sequence 72, Application US/10322673
is bublication No. US20030180296A1
igeneral INFORMATION:
i APPLICANT: Salcedo et al.
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US-10-322-673-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: human
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                       241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Rosen, Craig A
APPLICANT: Well, Fing
FILE REPERENCE: PF573
CURRENT APPLICATION WHORER: US/10/210, 793
FILE REPERENCE: PF573
CURRENT APPLICATION WHORER: 60/336, 695
PRIOR APPLICATION WHORER: 60/336, 695
PRIOR APPLICATION WHORER: 60/314, 381
PRIOR APPLICATION WHORER: 60/216, 879
PRIOR APPLICATION WHORER: 60/140, 908
PRIOR APPLICATION WHORER: 60/140, 908
PRIOR PLING DATE: 2000-03-08
PRIOR APPLICATION WHORER: 60/140, 908
PRIOR PLING DATE: 2000-03-08
PRIOR PLING DATE: 2000-
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          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                         121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                          181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                  181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                       241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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US-10-310-793-26
Sequence 26, Application US/10310793
Sublication No. US20030198640A1
GENERAL INFORMATION
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US-10-310-793-26
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US-09-652-287A-12
US-08-996-139-11
US-08-995-659-11
US-09-215-649A-11
US-09-577-780-11
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.5.2

SOFTWARE: Microsoft Word, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/670,354

FILING DATE: 25-UW-1996

CLASSIFICATION NUMBER: US 08/496,632

FILING DATE: 29-UN-1995

CLASSIFICATION NUMBER: US 08/548,368

FILING DATE: 01-NOV-1995

CLASSIFICATION ATA:

APPLICATION NUMBER: US 08/548,368

FILING APPLICATION: 435

ATORNEY/AGENT INFORMATION:

ANAE: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

RECISTRATION NUMBER: 2835-B

TELECOMMUNICATION INFORMATION:

TELEPAN: (206) 233-0644
                                                                      PCT-US96-10895-4
                                                                                                                                                                                               US-09-871-856-11
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TELEFAX: (ZC.)
TELEX: 756822
; INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TVPE: amino acid
TVPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-670-354-2
 Query Match
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Sequence 2, 7
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-88-08-10

US-09-333-593A-6

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US-09-919-033-2

US-09-919-033-2

US-09-919-033-2

US-09-919-03-1

US-09-918-03-1

US-09-918-03-1

US-09-918-03-1

US-09-918-03-1

US-09-320-424-11

US-09-825-563-11

US-09-825-563-13

US-09-825-563-13

US-09-825-563-13

US-09-825-563-13

US-09-825-63-13

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US-09-825-63-13

US-09-920-424-13

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US-09-920-424-13
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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No.
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Length 281;

DB 1;

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TITLE OF INVENTION: Apo-2 Ligand
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
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                   0; Indels
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100.0%; Pred. No. 3.5e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Abshenazi, Avi J.
TILE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION UNBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
                   0; Mismatches
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Patent No. 6046048
GENERAL INFORMATION:
Best Local Similarity 100.
Matches 281; Conservative
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TYPE: PRT
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US-08-584-031-1
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US-08-780-496-1
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APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

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61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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US-08-883-086-10

i Sequence 10, Application US/08883086

patent No. 6171787

general information:
   TITLE OF INVENTION:
   TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
   TORRESPONDENCES: 13
   CORRESPONDENCESS:
   ADDRESSE: Abbort Laboratories
   TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
   CORRESPONDENCESS:
   ADDRESSEE: Abbort Laboratories
   TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Abbort Laboratories
   TITLE OF INVENTION AND ADDRESS:
   ADDRESSEE: Abbort Park Road
   CITY: Abbort Park Road
   CITY: Abbort Park
   CONNITY: USA
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100.0%; Score 1478; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.5e-149.
Matches 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                          CLERALING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P0978P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MARCHARG, DIABNE L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0976
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/952-9416
TELEPAX: 415/952-9881
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNHEH, ALENGEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
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                                                                                                                                                                                                                                               Score 1478; DB 3;
Pred. No. 3.5e-149;
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100.0%; Score 1478; i
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 281; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT APPLICATION NUMBER: US/09/6.25
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR PILING DATE: 1997-03-14
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SOFTWARE: FastSEQ for Windows Version 3.0
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09333593A Patent No. 6313269
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ORGANISM: HOMO SAPIENS
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                                                                                                                                                                                ORGANISM: human
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LENGTH: 281
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TITLE OF INVENTION: CYLOKINE that Induces Apoptosis
TITLE OF INVENTION: CYLOKINE that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
FARLIER PPLICATION NUMBER: 09/190,046
EARLIER PILING DATE: 1998-11-10
EARLIER PILING DATE: 1998-03-26
FARLIER PILING DATE: 1998-03-26
EARLIER PILING DATE: 1996-06-25
EARLIER PILING DATE: 1996-06-25
EARLIER PILING DATE: 1996-06-25
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100.0%; Pred. No. 3.5e-149;
tive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POFEmbSki, Priscilla E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFAX: 847-938-2623
                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09320424; Patent No. 6284236; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: No. 6171787e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 281; Conservative
                       COMPUTER READABLE FORM:
60064-3500
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US-09-320-424-2
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APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/1320,424
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 09/190,046
PRIOR PILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 09/64,641
PRIOR APPLICATION NUMBER: 08/670,354
PRIOR PILING DATE: 1996-06-25
PRIOR FILING DATE: 1995-06-29
PRIOR FILING DATE: 1995-06-29
PRIOR FILING DATE: 1995-06-29
NUMBER: 08/670,324
PRIOR FILING DATE: 1995-06-29
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
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100.0%; Pred. No. 3.5e-149;
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Best Local Similarity 100.
Matches 281; Conservative
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US-09-919-039-118
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                            61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                  RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                            FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
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ADDRESSEE: Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
                                                                                                                                                                                                                                                    SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
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100.0%; Pred. No. 3.5e-149;
iive 0; Mismatches 0;
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US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNP-Related Death Ligand
; WUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KETBET, LOTI L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 281; Conservative
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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STATE: MI
COUNTRY:
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Best Local Similarity 100.
Matches 281; Conservative
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ORGANISM: Homo sapiens
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US-09-934-465-1
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TYPE: PRT
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             APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0015 US CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT APPLICATION NUMBER: 00/222,113

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL PROGram

SEQ ID NO 118

LENGTH: 281
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100.0%; Pred. No. 3.5e-149;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09582450
; Patent No. 6740739
; GRERAL INPORMATION:
; APPLICANT: Achley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Pitti, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
FILE REFERENCE: P0978P4
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US/9/582,450
; CURRENT FILING DATE: 1998-01-15
; PRIOR FILING DATE: 1998-01-15
; NUMBER OF SEQ ID NOS: 17
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-582-450-1
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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100.0%; Pred. No. 3.5e-149;
ative 0; Mismatches 0;
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Sequence 4, Application US/10011125A
Patent No. 6928121
GENERAL INFORMATION:
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Query Match 100.0%; Score 1478; DB 5; Best Local Similarity 100.0%; Pred. No. 3.5e-149; Matches 281; Conservative 0; Mismatches 0;
                       TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 75682
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
        TELECOMMUNICATION INFORMATION
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: HOMO SAPIENS
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US-09-072-993C-3
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                                                                                                                                                                                                                                                                     100.0%; Score 1478; DB 4; Length 281; 100.0%; Pred. No. 3.5e-149; ive 0; Mismatches 0; Indels 0
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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; TITLE OF INVENTION: BACTERIAL HOST STRAINS; FILE REFERENCE: P1804R1
; CURRENT APPLICATION WUMBER: US/10/011,125A; CURRENT FILING DATE: 2001-12-07; PRIOR APPLICATION NUMBER: US 60/256,162; PRIOR FILING DATE: 2000-12-14; NUMBER OF SEQ ID NOS: 12
; LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh COMPUTER: Apple Macintosh CERATING SYSTEM: Apple 7.5.2 SOFTWARE: Microsoft Word, Version 6.0.1 CURRENT APPLICATION DATA: PCT/US96/10895 FILLING DATE: 25-JUN-1996
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APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANGENERON, KAEHNYN A.
REGISTRATION NUMBER: 23,172
REFERENCE/DOCKET NUMBER: 2835-WO
                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 281; Conservative
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ZIP: 98101
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                                                                                                                                                                                         TYPE: PRT
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Sequence 3, Application US/09072993C
; Sequence 3, Application US/09072993C
; Patent No. 6346386
; GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Michael R. Brigham-Burke
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANYAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
FILE OF INVENTION: ANYAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
FILE OF INVENTION: ANYAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
FILE OF INVENTION: ANYAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
CURRENT APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/055,550
PRIOR APPLICATION NUMBER: 60/055,550
; PRIOR APPLICATION NOWER: 60/057,550
; NUMBER OF SEQ ID NOS: 9
; SCO ID NO 3
; SEQ ID NO 3
; LENGTH: 279
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                                                                                                                                                                                                                                   DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                     61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                     RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                       121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLAMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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Length 281;
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                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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YIYSQTYPRPQEEIKENTKNDKQMVQYIYKYTSYPDDILLAMKSARNSCWSKDAEYGLYSI 242
                                                                                                                                     131 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYXIXSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 FYYIYSQTYFRFQEEIKENTKUDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 250
61 SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 83.8%; Score 1238; DB 4; Length 271; Best Local Similarity 85.4%; Pred. No. 1.3e-123; Matches 240; Conservative 2; Mismatches 5; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----IDMDHEASFFGAFLVG 271
                                                                                                                                                                                                                241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
                                                                                                                                                                                        243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                    RESULT 15
US-09-569-611C-30
| Sequence 30, Application US/09569611C
| Patent No. 6720182
| GENERAL INFORMATION:
| APPLICANT: SAVITZKY et al.
| TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
| CURRENT APPLICATION NUMBER: US/09/569,611C
| CURRENT APPLICATION NUMBER: US/09/569,611C
| NUMBER OF SEQ ID NOS: 52
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 300
| LENGTH: 271
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ORGANISM: Homo sapiens
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Search completed: June 22, 2005, 06:02:15 Job time : 33.1756 secs

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June 22, 2005, 05:57:23 ; Search time 23.187 Seconds (without alignments) 1008.352 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
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US-10-662-429-2_COPY_39_281 1287 1 TNELKQMQDKYSKSGIACFLNEHLIDMDHEASFFGAFLVG 243	BLOSUM62 Gapop 10.0 , Gapext 0.5
Title: Perfect score: Sequence:	Scoring table: BLOSUM62 Gapop 10

• .	283416
residues	Total number of hits satisfying chosen parameters:
16763	chosen
283416 seqs, 96216763 residues	satisfying
28341	hits
ed:	number of
Searched	Total

	\$ summaries
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2000000000	Match 0% Match 10 first 45
90	E E E
length: length:	. Minimum Maximum Listing
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Minimum Maximum	t - p;
Min Max	Pos

Listing first	PIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	
	Database :	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Fas ligand - mouse	Fas ligand - human	fas ligand - rat	CD40 ligand - bovi	CD40 ligand - mous	CD40 ligand - huma	118	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	lymphotoxin - bovi	tumor necrosis fac	tumor necrosis fac	lymphotoxin alpha	tumor necrosis fac	tumor necrosis fac		00		tumor necrosis fac	tumor necrosis fac		. tumor necrosis fac	lymphotoxin-beta -	tumor necrosis fac	mRNA maturase b14	amphotropic murine	u	tumor necrosis fac
SUMMARIES	ат	A53062	138707	A49266	253090	S21738	153476	S17289	A25451	S12606	I54490	S24641	JQ1344	OWHUN	QWHUX	OWMSN	JU0029	S22052	JH0529	806192	B27303	S52715	S24642	JN0869	I49139	JH0309	QQBY2M	I48083	0	S11688
	DB	. ~	N	~	N	~	N	-	-		~	-	-	-	-	-	~	-	-	~	-	~	-	-	7	-		~	7	7
	Length	279	281	278	261	260	261	204	234	232	235	204	234	233	205	235	235	233	234	193	202	185	233	202	306	197	638	652	244	233
de	Query Match	14.7	14.2	13.8	11.8		•	10.5	•			•	•	•	9.5	4.6	•	9.3	9.1	9.0	8.9		8.8	8.7	8.4		8.2	•	7.9	7.7
	Score	189.5	182.5	177.5	152	138.5	137	134.5	131.5	130	129.5	127.5	126	123	122	121	121	120	117.5	115.5	114	113.5	113	111.5	108.5	107	105	102.5	102	98.5
	Result No.	7	7	m	4	Ŋ	9	7	80	a	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		56			29

protein kinase, pr	hypothetical prote	chromodomain helic	heat shock transcr	cardiac muscle fac	probable membrane	DNA ligase homolog .	hypothetical prote	myosin-light-chain	NBS-LRR type resis	alpha-N-arabinofur	FAB1 protein - yea	DNA-directed DNA p	protein C47E8.8 [i	hypothetical prote	mitogen-activated
F95122	G95104	T23056	A31593	T29095	AB1658	T14707	T15010	JN0583	T03031	B59296	S56274	S56278	E89303	T31473	JC5153
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448	455	1465	833	1538	865	345	365	1176	313	328	2278	611	1425	1675	826
7.6	7.4	7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.0	6.9	6.9	6.9	6.9	6.9	6.8
97.5	95	93	92.5	92.5	92	91	91	91	89.5	89	89	88.5	88.5	88.5	88

ALIGNMENTS

RESULT 1 A53062 Fas ligand - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #text_change 09-Jul-2004 C;Accesion: A53062 R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag Cell 76, 969-976, 1994 A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A;Reference number: A53062; MUID:94185175; PMID:7511063 A;Accession: A53062 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-279 <tak>A;Cossione: C;Cossione: C;Co</tak>	Query Match 14.7%; Score 189.5; DB 2; Length 279; Best Local Similarity 25.8%; Pred. No. 1.2e-08; Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;	QY 45 QLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 104	Qy 105 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSGTYFRQEEIKENTKN 164	OY 165 DKOMVQYIY-KYTSYPDPILLMKSAR-NSCMSKDAEYGLYSIYQGGIFELKENDRIFVSV 222 :::: :: :: :	Qy 223 TNEHLIDMDHEASFFGAF 240 : : : : Db 260 SQLSLINFEESKTFFGLY 277	RESULT 2 138707 Fae ligand - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 138707; J22340; S57565; J38554 C;Accession: 138707; J394 R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S. Int. Immunol. 6, 1567-1574, 1994 A;Title: Human Fas ligand; gene structure, chromosomal location and species specificity. A;Reference number: 138707 A;Reference number: 138707 A;Accession: 138707 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-281 cRES A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:95954

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216 DRIFVSVTNEHLIDMDHEASFFG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
                                                                                                                                                                                                                                                                                                                                                                                              275 LY 276
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S21738
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cispecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cispecies: 17-Jule-1993
T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266
A;Reference number: A49266
A;Reference number: A9266
A;Residus: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 eSUD>
A;Residues: 1-278 eSUD>
A;Cross-references: UNIPROT: P36940; GB:U01470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C;Keywords: glycoprotein; transmembrane protein
     H
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                                                                                                                                                                                                           Rischatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A; Reference number: $57565
A; Reference number: $57565
A; Status: preliminary
A; Residues: 1-281 - <6CHs
A; Cross-references: EMBL: X89102; NID: 9887455; PID: 9887456
R; Aiderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; CA; Caxp. Med. 181, 71-77, 1995
A; Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A; Reference number: 138554; MUID: 95105731; PMID: 7528780
                                                                                                                                                                                     A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biochem. Batophs. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 MP-----LEWEDT-YGIVLLSGVKYKKGGLVINETGLYPVYSKVYFRGQ---- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 ENTKNDKQMVQYIY-KYTSYPDPILLMKSARNS-----CWSKDAEYGLYSIYQGGIFEL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 --SCNNLPLSHKVÝMRNSKÝPQDLVMMEGKMMSYCTTGQMWAR-----SSÝLGAVFNL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 WQLRQLVRKMI-LRTSEETISTVQEKQQNI---SPLVRERGPQRVAAHITGTRGRSNTLS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-281 <REZ>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane #status predicted <TMM>
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: 138554
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 KENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                               A; Molecule type: DNA
A; Residues: 1-281 <MIT>
                                                                                                            Accession: JC2340
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Cispecies: Mus musculus (house mouse)
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                                                                                                                 ----EWEDT- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 SSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYIYSQTYFRFQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 EEIKENTKUDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S15.C; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: $53090
                                                                                                                                                                                                                                                                                                                            163 YGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ-----SCNSQPLSHKVYMRNFKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 CEEIRSRPEDLV-YDIMQNXE-----VKKKEKNFEMHKGDQEPQ-IAAHV-----I
                                                                                                                                                                                                                                          SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQBEIKENTKNDKQMVQYIY-KYTSYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 DPILLIMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 CWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL
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Best Local Similarity 27.1%; Pred. No. 1.7e-05;
Matches 55; Conservative 39; Mismatches 77; Indels
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Rikuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: $17289; WUID:91340150; PMID:1874444
A;Accession: $17289
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N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A55454; A25451; J$0727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H. DNA S, 149-156, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: DNA
A; Residues: 1-204 <KUH>
A; Residues: 1-204 <KUH>
A; Cross-references: UNIPROT: P26445; EMBL: X54859; NID: g2132; PIDN: CAA38638.1; PID: g2133
C; Genetics:
A; Introns: 32/3; 68/1
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F; 1-33/Domain: signal sequence #status predicted <SIG>F; 34-204/Product: tumor necrosis factor beta #status predicted <MAT>
                                                                                                          11;
                                                                                                                                                                                                                 89 -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 SSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYIYSQTYFRFQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 EEIKENT-----KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQG 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 WESSRSGHSFLSNLHLRNGELVIHEKGPYYIYSQTYPRFQEEIKENTKNDKQMVQYIYKY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 REASSQAPFIASLCLKSPGRFER------ILLRAANTHSSAKPC--GQQSIHLG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
                                                                                                                                                                          39 CWQVXWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S17289
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                                                                                                              Gaps
                                                                                                          48;
                                                                                                       73; Indels
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                                   Query Match
10.6%; Score 137; DB 2;
Best Local Similarity 24.6%; Pred. No. 0.00033;
Matches 52; Conservative 38; Mismatches 73.
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Best Local Similarity 24.7%; Pred. No. 0.00039;
Matches 46; Conservative 31; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 GIFELKENDRIFVSVTNEHLIDMDHEASFFG 238
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A; Residues: 1-261 <HOL>
A; Residues: 1-261 <HOL>
A; Cross-references: UNTRROT: P29965; EMBL: Z15017; NID: 938483; PIDN: CAA78737.1; PID: 938484
R; Spriggs, M.K.; Armitage, K.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A; Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobuli
A; Reference number: JH0793; MUID: 93094757; PMID: 1281209
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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand fo A;Reference number: S28017; WUID:93049181; PMID:1385114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
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A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy,
FEBS Lett. 315, 259-266, 1993
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of
A;Reference number: S28852; MUID:93138085; PMID:7678552
                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                        SSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYFRFQE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 EIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEND 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 E----PSSORPFIVGLWLKPSIGSERILLKAANTHSSSOLCEQ--OSVHLGGVFELQAGA 234
                                                                                                                                                                                                      39 CWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 98
                                                                                                                                                                                                                                                                          84 CEEMRROFEDLVKDITLNK-------BEKKENSFEMORGDEDPOIAAHV-----V
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A;Accession: JH0793
A;Molecule type: mRNA
A;Residues: 1-261 - 4SPR->
A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Bur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S26694; MUID:93076854; PMID:1280226
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F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                          31;
F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                          DB 2; Length 260;
                                                                                                                                       Indels
                                                               Query Match 10.8%; Score 138.5; DB 2; Best Local Similarity 25.1%; Pred. No. 0.00024; Matches 47; Conservative 37; Mismatches 72;
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C,Keywords: glycoprotein; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 RIFVSVT 223
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235 SVFVNVT 241
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A; Molecule type: mRNA
A; Residues: 1-261 <GAU>
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A; Residues: 1-261 <GRA>
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07:29:38

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porcine tumor necrosis fac

PID:92134 as Gly

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Ajfutrons: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Superfamily: propeptide #status predicted <PRO>
F;1-7/Domain: propeptide #status predicted <PRO>
F;18-222/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                    A;Accession: S18955
A;Molecule type: mRNA
A;Residues: 1-23 - CCHO.
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A;Reference number: 146659; MUID:90034181; PMID:2478420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C;Genetics:
                                                                 A;COSS-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PI A;Note: the authors translated the codon GAG for residue 202 as R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murteaugh, M.P. submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding A;Reference number: $18965
                                          A; Residues: 1-232 < KUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: PlINF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '; Superfamily: tumor necrosis factor
'; Superfamily: tumor necrosis factor
'; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb.
'; Bal/Domahi: propeptide #status predicted <PANT>
'; B-234/Product: tumor necrosis factor #status predicted <PANT>
'; B-234/Product: tumor necrosis (actor #status predicted <PANT>
'; B-234/Product: myristate (Lys) (covalent) #status predicted
'; B3/Binding site: myristate (Ser) (covalent) #status predicted
'; B3/Binding site: producted predicted
                                                                                                           A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MINDA
B; Molecule type: Milecule type
A; Molecule type
A; Molecule type: Milecule type
A; Molecule type
A; Mile: Molecule type
A; Molecule type: MIND: 86219712; MIND: 3519138
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A; Residues: 1-232 <DNE>
A; Residues: 1-232 <DNE>
A; Cross-references: UNIPROT: P23563; EMBL: X54001; NID: g2135; PIDN: CAA37949.1; PID: g2136
A; Cross-references: UNIPROT: P23563; EMBL: X54001; NID: g2135; PIDN: CAA37949.1; PID: g2136
B; Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A; Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A; Reference number: S17289; MUID: 91340150; PMID: 1874444
   for rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: this sequence differs from that shown in having a Gln inserted between residues R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A. Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-A;Reference number: JH0309; MUID:91065534; PMID:2249779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
G; Genetics: 62/3; 80/1; 96/1
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Superfamily: propeptide #status predicted <PRO>
F; 82-234/Product: tumor necrosis factor #status predicted <MAT>
A,Title: Molecular cloning and expression in Escherichia coli of the cDNA coding A,Reference number: A25454; MUID:86219711; PMID:3519137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NPQVEGQL-----OWLSQRANALLANGMKLTDNQLVVPADGLYLIY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIY 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 SQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLMKSARNSCWSKDAEYG----L 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S12606; S17290; S18965; 146659
R;Drews, R.T.; Coffee, B.W.; Pretwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene Sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNDEESMINSPCWQVKWQLRQLVRKMI-LRTSEETISTVQEKQQNISPLVRERGPQRVAAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%; Score 131.5; DB 1; Length 234; Best Local Similarity 22.9%; Pred. No. 0.00084; Matches 50; Conservative 36; Mismatches 79; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 EPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGGVYFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 VVA-----
                                                                                                                                                                                                                                                                                                                                                                         A, Accession: A25451
A, Molecule type: DNA
A, Residues: 1-234 <IT2>
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                                                                         A; Accession: A25454
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R;Crew, M.D.; Filipowsky, M.E.
Immunogenelics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucc
A;Reference number: I54490; MUID:92218012; PMID:1348497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT: P36939; GB: M59233; NID: g202506; PIDN: AAA40596.1; PID: g202507
                                                                        9
                                                                                                                              80 GPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 136
                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                     124 VVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQ 177
                                                                                                                                                                                                                                             137 VIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCW 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 154490
                                                                                                                                                                                          66 GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL
                                                                        20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           194 SK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 232;
10.1%; Score 130; DB 1; Lengua 25.1%; Pred. No. 0.0011; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.1%; Score 129.5; DB 2; 24.5%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: I54490
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-215 <RES>
                  Query Match 10.1%; Score 130; DB Best Local Similarity 25.1%; Pred. No. 0.00 Matches 43; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Aintrons: 67/3; 79/1; 95/1

C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;F78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PJ R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka, Mature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NPkappaB family within a A;Reference number: S36152; MUID:93272029; PMID:8499947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R'Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A., Nature 312, 724-729, 1984
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to l; A,Reference number: A93351; MUID:85086244; PMID:6392892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-233 <PEN>
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Cross-references: GB:X02101; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Science 228, 149-154, 1985
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C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 09-Jul-2004
C;Accession: A93585; S36153; A3351; A44189; B61478; I53311; S62610; I54522; A01646; B237; R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D Nucleic Acids Res. 13, 6361-6373, 1985
     A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245 C;Comment: This protein is an important proximal mediator of endotoxemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor. A;Reference number: A44189; MUID:85142190; PMID:3856324 A;Accession: A44189 A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ISTYQEKQ----QNISPLVR----ERGP-QRVAAHITGTRGRSNTLSSPNSKNEKALG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 IGPQREEQLPNAFQSINPLAQTIRSSSRTPSDKPVAHVVA-------NPQAEG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 RKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 YIYKYT-----SYPDPILLMKSARNSCWSKDAEYG----LYSIYQGGIFELKENDRIF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 126; DB 1; Length 234; 22.5%; Pred. No. 0.0025; ve 35; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               umor necrosis factor alpha precursor [validated] - human
Alternate names: cachectin; TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P,146-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.5%;
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Matches 45; Conservative
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A; Residues: 1-233 <NED>
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(Species: Equue caballus (domestic horse)
()Species: Equue caballus (domestic horse)
()Accession: J01344
R.Su, X.; Morris, D.D.; McGraw, R.A.
(Species: 10.319-311, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis
A;Reference number: J01344; MUID:92084125; PMID:1748301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
                                                                                                                                                                                                                                                                                                                                                          ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                             SPLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 173
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                                                                                                          ----SSRSGH
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9.9%; Score 127.5; DB 1; Length 2
Best Local Similarity 24.9%; Pred. No. 0.0015;
Matches 47; Conservative 29; Mismatches 78; Indels
     75;
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Mismatches
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tumor necrosis factor alpha precursor
39;
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A; Residues: 1-204 <CL2>
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A; Molecule type: DNA
A; Residues: 1-234 <SUX>
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228 VYFG 231
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C; Superfamily: tumor 1
45;
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Matches
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07:29:38 2005

Wed Jun 22

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lymphotoxin alpha precursor - human Nighternate names: Lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
N;Alernate names: Lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 07-Jul-1995 #text change 09-Jul-2004
C;Accession: A92755; S36154; IS4482; A93350; B32877; A91906; A61478; S26951; A01645; A23;
E;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel, J. Cell. Biochem. 29, 171-181, 1985
A;Title: Structure and chromosomal localization of the human lymphotoxin gene.
A;Reference number: A92755; MUID:86086150; PMID:3001109
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A,Status: translated from GB/EMBL/DDBJ
A,Status: translation not shown; translated from GB/EMBL/DDBJ
A,Status: translation not shown; translated from GB/EMBL/DDBJ
A,Wolecule type: DNA
A,Rolecule type: DNA
A,Rossiques: 1-124,'P',126-205 <RES>
A,Cross references: GB:MS5913, NDD:9339742; PIDN:AAB59455.1; PID:g339743
A,Experimental source: ancestral haplotype 8.1)
R,Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.;
Nature 312, 721-724, 1984
A;Title: Cloning and expression of CDNA for human lymphotoxin, a lymphokine with tumour r
A;Reference number: A93350; MUID:85086243; PMID:6334807
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A,Residues: 35-205 <GOE>
R;Kobayashi, Y; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Blochem. 100, 727-733, 1986
A;Fitle: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hyk
A;Reference number: A91906; MUID:87057135; PMID:3536896
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A;Molecule type: mRNA
A;Residues: 1-59, NV,61-205 <KOB>
A;Cross.references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue 1
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A; Residues: 1-205 <GRA>
A; Cross-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
A; Experimental source: Lymphoblastoid cell line RPMI-1788
R; Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A; Fitle: Tumor necrosis factors: gene structure and biological activities.
A; Reference number: A32877; MUID:87217059; PMID:3472740
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Nature Genet. 3, 137-145, 1993
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A; Residues: 1-12, R', 14-205 < IRI>
A; Residues: L-12, R', 14-205 < IRI>
A; Residues: L-12, R', 14-205 < IRI>
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992 R; Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A; Title: Haplotypic polymorphisms of the TNFB gene.
A; Reference number: 154482; MUID:91139175; PMID:1671667
----GCPSTHVLLTHTISRIAVS 162
                                                                                                                                                              178 YPDPILLMKSARNSCWSK----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH
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     112 LLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ----
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Residues: 1-59,'N',61-205 <NED>
Cross-references: UNIPROT:P01374
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A; Residues: B9-102;109-119;121-128, X', 130-131;142-144, X', 146, XXX', 150-152;159-174;180

R; Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,

Bur. J. Blochem. 152, 515-522, 1985

A; Title: Molecular cloning and expression of human tumor necrosis factor and comparison

A; Reference number: 153311; MUD:86030296; PMID:393069

A; Reference number: Lanalated from GB/EMBL/DDBJ

A; Residues: 1-233 < MAR>
A; Residues: 1-233 < MAR>
A; Residues: 1-233 < MAR>
A; Reference number: S62610; MUD:96202967; PMID:8631363

A; Reference number: S62610; MUD:96202967; PMID:8631363

A; Residues: 77-99 < TAR>
A; Residues: 77-99 < TAR>
A; Residues: 77-99 < TAR>
A; Residues: 1-50 < TARA
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R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
B;Stevenson, P.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
B;Stevenson, Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
A;Contents: annocation; dentification of myristylated lysines
B;Agarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring
J; Biol. Chem. 260, 2345-2354, 1995
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Contents: annocation; disulfide bond
A;Contents: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells: It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and -bera (lymphotoxin) are the products of different genes closely ut are produced by different cell types and have different induction kinetics.
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C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
F;1-76Dmain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
                                                      A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
                                                                                                                                                                                                                    -beta and
                                                                                                                                                                                                               A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, A;Reference number: A61478; MUID:88301617; PMID:2841543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .24 SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKOMVQYIYKYT----S 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;145-177/Disulfide bonds: #status experimental
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A,Cross-references: GDB:120441; OMIM:191160
A,Map position: 6521.3-6521.3
A,Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
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Matches 43; Conserv
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Molecule type: mRNA
Residues: 1-230,'R',232-235 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-235 < SEM>
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R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Pujii, M.; Masaki, N.; Nakamura, K.I.; An Liymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Recession: A61478
A;Molecule type: protein
A;Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1 K;Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
A;Riciatio: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation
C; Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
while having no detrimental effect on normal cells. It can also act synergistically wit
C; Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ
ical activities but are produced by different cell types and have different induction ki
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A; Accession: A22908
A; Accession: A22908
A; Accession: A22908
A; Residues: 1-235 < SHI>
A; Cross-references: UNIPROT:P06804; GB:M20155
A; Cross-references: UNIPROT:P06804; GB:M20155
B; Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A; Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl A; Reference number: S03791; MUID:87298639; PMID:3040015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E
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Artile: N-linked sugar chain structure of recombinant human lymphotoxin produced by A;Reference number: S34742; MUID:93311995; PMID:8323280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage F;1-34/Domain: signal sequence #status predicted <SIG>P:15-05/Product: lymphotoxin #status predicted <MAT>P:15-105/Product: lymphotoxin #status predicted <MAT>P:141/Binding site: carbohydrate (Thr) (covalent) #status experimental F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Jul-2004
C;Accession: A22908; S03791; Ā27303; A25164; A23127; A34251; I59058; A36696
B;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:120442; OMIM:153440
A;Map postition: 5251.3-6p21.3
A;Introns: 33/3; 69/1
A;Note: the first intron occurs before the initiator codon
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A,Molecule type: protein
A,Residues: 35-59,'N', 61-205 <VOI>A,Note: 60-Thr was also found
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Best Local Similarity 23.4<sup>†</sup>
Matches 37; Conservative
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A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nec; A;Reference number: A93679; MUID:88067722; PMID:3684584
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R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. US.3A. 82. 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coll of the CDNA for murine tumor necrosis A;Reference number: A25164; MUID:85298296; PMID:3898078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-235 <PEN>
A; Cross-references: GB:M11731; NID: 9202084; PIDN: AAA40458.1; PID: 9202085
A; Cross-references: GB:M11731; NID: 9202084; PIDN: AAA40458.1; PID: 9202085
R; Fransen: L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, F
Nucleic Acids Res. 13, 4417-4429, 1985
A; Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expres
A; Reference number: A23127; MUID: 85242112; PMID: 2989794
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,Residues: 70-87 cCSE>

,Coput, D. Beutler, B., Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.

roc. Nall. Acad. Sci. U.S.A. 83, 1670-1674, 1986

,Title: Identification of a common nucleotide sequence in the 3'-untranslated region of

,Reference number: I59058; MUID:86149365; PMID:2419912
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Aintrons: 62/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3; 81/3;
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;Residues: 1.235 cRRA>
;Cross-references: GBX KO2611; NID:954844; PIDN:CAA26457.1; PID:954845
;Cross-references: GBX K.; Beutler, B.
;Cseh, K.; Beutler, B.
*Biol.** Chem. 264, 16256-16260, 1989
;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
;Reference number: A34251; MUID:89380231; PMID:2777790
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                                                                                                                                  R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
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A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A;Note: article in Russian with English abstract
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112 ANALLANGMDLKDNQLVVPADGLYLVYSQVLFKGQ-----GCPDYVLLTHTVSRFAISYQ 166
                       180 DPILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE 233
 8 6 6 6 6
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	:: :: :: :: :: :: :: :: :: :: :: :: :	167 EKVNILSAVKSPC-PKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAES 225
· · · · · · · · · · · · · · · · · · ·	<u>:</u>	VNLL
	••	ZEK

²³⁴ AS-FFG 238 :|| 226 GQVYFG 231

Search completed: June 22, 2005, 06:03:13 Job time: 24.187 secs

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June 22, 2005, 05:57:23 ; Search time 100.168 Seconds (without alignments) 1242.266 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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US-10-662-429-2_COPY_39_281 1287 1 TNELKQMQDKYSKSGIACFL.....NEHLIDMDHEASFFGAFLVG 243

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence:

Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	91	Q8k3g0 rattus norv		Q7tlf2 gallus gall				Q90wt9 gallus gall	Q6jsd9 homo sapien	Q9ese2 r tumor nec	035235 m tumor nec	014788 h tumor nec	P41047 mus musculu	Q9bdn1 cercocebus	Q7tmv9 mus musculu	P63308 macaca fasc	P63307 macaca mula	P63306 macaca neme	P48023 homo sapien	Q9bea8 sus scrofa	Q8k3y8 mus musculu		Q861w5 felis silve	Q9wv90 marmota mon	Q80yz0 mus musculu		Q9i8d8 gallus gall		Q6j3q6 canis famil	095150 homo sapien	043557 homo sapien
SUMMARIES	ΩI	TN10 HUMAN	Q8K3 <u>G</u> 0	TN10 MOUSE	Q7T1 <u>F</u> 2	Q6DHG9	67ZZX9	Q9DDZ5	Q90WT9	Q6JSD9	TN11 RAT	TN11 MOUSE	TN11_HUMAN	TNF6_MOUSE	TNF6_CERTO	Q7TIMV9	TNF6_MACFA	TNF6 MACMU	TNF6 MACNE	TNF6_HUMAN	TNF6_PIG	Q8K3 <u>Y</u> 8	TNF6_RAT	Q861W5	Q9WV90	QBOYZO		TNF5_CHICK	Q8NFE9	Q6J3Q6	TN15_HUMAN	TN14_HUMAN
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•	Query Match	100.0	68.3	7	54.7	40.1	23.9	23.7	23.7	22.6	19.5	18.5	18.3	14.7	14.4	14.3	14.3	14.3	14.3	14.2	14.1	14.0			13.6	13.6	13.4	13.3	12.9	12.7	12.4	12.4
	Score	1287	879	863	703.5	515.5	307.5	305.5	305	291	250.5	238.5	235.5	189.5	185.5	184.5	183.5	183.5	183.5	182.5	182	180	177.5	176.5	175.5	175	173	171	166	163.5	160	159.5
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QBmj19 macaca mula Q9qyh9 mus musculu	C71743 Cyptinus ca C70332 mesocricetu C60817 lateolabrax	Q8aw02 cyprinus ca Q9bdm3 aotus trivi Q9bdn3 callithrix	Q80xa4 peromyscus Q6t9c7 brachydanio P27548 mus musculu	P63305 cercocebus P29965 homo sapien
Q8MJ19 TN14_MOUSE	1/1/20 070132 060817	Q8AW02 TNF5 AOTTR TNF5-CALJA	Q80XA4 Q6T9C7 TNF5 MOUSE	TNF5_CERTO TNF5_HUMAN
211	1000	ичч	~ ~ ~	
239	227 227 216 241	231 261 261	232 234 260	261
12.2	11.2	11.0 10.9 10.9	10.7	10.6
152.5	151.5 144.5 143	141 140 140	137.5 137.5 137.5	137
332	335	8 6 6 8 6 0	4 4 4 3 2 3	4 4 5

ALIGNMENTS

RESU TN10 ID AC	RESULT 1 IN10 HUMAN ID TN10 HUMAN AC PS0591; OT 01-OCT-1996	STANDARD; (Rel. 34, Cr	RD; Created)	PRT;	281	AA.	
55	01-0CT-1996	(Rel. 34,	Last s	sedneuce .nbdate)	updat	te)	
D B	25-OCT-2004 Tumor necros	(Rel. 45, is factor	Last a liqand	nnotatio	ni up	25-OCT-2004 (Rel. 45, Last annotation update) Tumor necrosis factor ligand superfamily member 10 (TNF-related	ated
DE	apoptosis in	ducing lie	gand) (TRAIL pr	oteir	n) (Apo-2 ligand) ((Apo-2L).
S S	Name=TNFSF10; Synonyms=APO2L, TRAIL; Homo sapiens (Human).	; Synonym; (Human)	s=APO2L	, TRAIL;			
8	Eukaryota; Metazoa;	etazoa; Cl	Chordata;	, Crania	ca;	Craniata; Vertebrata; Buteleostomi;	stomi;
8	Mammalia, Eu	theria, P	Primates;	, Catarr	hini	; Hominidae; Homo.	
X Z	NCBI_TaxID=9606;	909					
R P	SEQUENCE FROM	M N.A.					
2	MEDLINE=9611	1955; Pub	Med=877	7713; DO	I=10	.1016/1074-7613 (95)	90057-8;
\$ \$	Nicholl J.K.	Schooley Sutherly	A., SEEC and G.R	Tak P.U. Davis	Smit	Wiley S.K., Schooley K., Smolak P.J., Din W.S., Huang CF., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A	Smith C.A.,
æ	Goodwin R.G.					•	
RŢ	"Identificat	ion and cl	haracte	rization	οŧ	"Identification and characterization of a new member of the TNF family	TNF family
Z.	that induces apoptosis.";	apoptosi	. (
7 E	Immunity 3:6	73-682(19	. (56				
2 0	SECTENCE FROM N A	4 2					
, ₂	TISSUE=Placenta;	nta;					
ă	MEDLINE=9627	8649; Publ	Med=866	3110; DO	1=10	MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687	687;
æ	Pitti R.M., 1	Marsters :	S.A., R	uppert S	ă :	S., Donahue C.J., Moore A.,	Α.,
8	Ashkenazi A.	•••	•	,			
ж Е	"Induction o	t apoptos.	is by A	po-2 119	and,		the tumor
X 5	necrosis rac	cor cytok.	1ne ram	00(1006)		necrosis ractor cytokine ramily."; .T Biol Cham 271.12687_12600/1006)	
2	[3]			(0)			
RP	SEQUENCE FROM N.A.	M N.A.					
2	TISSUE=Lymph;	••					
2	MEDLINE=2238	8257; Publ	Wed=124	77932; D)I=1(MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899	66;
\$ 5	Strausberg R	.L., Feing	gold E.	A., Grou	96. J	.H., Derge J.G.,	5
5 5	Altechul S.F	Zeeber		uetow K.	· ·	Schaefer C.F., Bhat	N.K.,
\$	Hopkins R.F.	, Jordan	., Moo	re T., M	S X	.I., Wang J., Hsieh	
æ	Diatchenko L	., Marusi	na K.,	Farmer A	Ä.	Rubin G.M., Hong L	:
& :	Stapleton M.	, Soares	ш ш ш	onaldo M	ر د د	Casavant T.L., Sch	eetz T.E.,
\$ 5	Brownstein M	omiellano	, a	Togniyu Petera G	י כי	brameon P D Mil	laby c.,
\$ \$	Bosak S.A.	McEwan P.	J. MCK	ernan K.		Malek J.A., Gunarati	ne P.H.,
æ	Richards S.,	Worley K	.с., на	le S., G	arcia	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.	ulyk S.W.,
æ	Villalon D.K	., Muzny	D.M., S	odergren	Μ	., Lu X., Gibbs R.A	
æ	Fahey J., He	lton E.,	Kettema	n M., Ma	dan 7	A., Rodrigues S., Sa	anchez A.,
8 5	Whiting M.,	Madan A., W Tonch	Young	A.C., Sh	evch e	enko Y., Bourtard G	·
5 2	Rodriguez A.	Grimme	יייי בייי	Schmutz		Myers B.M.	
2	Butterfield	Y.S.N., K	rzywins	ki M.I.,	Ska	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	Β.,
\$	Schnerch A.,	Schein J	.E., Jo	nes S.J.		Marra M.A.;	
RT	"Generation	and initia	al anal	ysis of	поте	than 15,000 full-lo	ength human

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R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0005102; F:receptor binding; TAS.
R GO; GO:0007267; P:cell-cell signalling; TAS.
R GO; GO:00043123; P:postive regulation of I-kappaB kinase/NF-k. .; IEP.
R GO; GO:0007165; P:signal transduction; TAS.
R GO; GO:0007165; P:signal transduction; TAS.
R InterPro; IPR008983; TNF family.
R InterPro; IPR008983; TNF family.
R InterPro; IPR008363; TNF milke.
R PFG0029; TNF; 1.
R PRODOM; PD002012; TNF; 1.
R PROSITE; SG0251; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            X-XAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
Sung Y.C., Oh B.-H.;
"2.8 A resolution crystal structure of human TRAIL, a cytokine with
selective antitumor activity.";
Immunity 11:253-261(1999).
ITMPRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10B/TRAILR1,
TNFRSF10B/TRAILR2, TNFRSF10B/OFG. Induces apoptosis Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OFG that cannot
                                                              MEDLINE=20017054; PubMed=10549268; DOI=10.1016/S1097-2765(00)80207-5; Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.; "Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5."; Mol. Cell 4:563-571(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        per
                                                                                                                                                                                              PubMed=10542098; DOI=10.1038/14935; Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones B.Y., Screaton G.R.; Screaton G.R.; Screaton G.R.; Screaton G.R.; Screaton G.R.; Screaton G.R.; Studiture of the TRAIL-DFS complex reveals mechanisms conferring specificity in apoptotic initiation."; Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      induce apoptosis.
COFACTOR: Binds 1 zinc ion and one anionic solvent molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and prostate. SIMILARITY: Belongs to the tumor necrosis factor family.
             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281
                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, BC03272; AAH32722.1; --
PDB; 1D0G; X-ray; A/B/D=114-281.
PDB; 1D40; X-ray; A=114-281.
PDB; 1D40; X-ray; B=119-281.
PDB; 1D66; X-ray; B=119-281.
PDB; 1D3; X-ray; D/E/F/J/K/L=114-281.
Genew; HGNC:11925; TNFSF10.
H-InvDB; HIX0003863; --
MIM; 603598; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U37518; AAC50332.1; -. EMBL; U57059; AAB01233.1; -.
mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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PROSITE; PS50049; TNF 2; 1.
3D-etructure; Apoptosīs; Cytokine; Metal-binding; Signal-anchor; Transmembrane; Zinc.
1 Cytoplasmic (Potential).
                                             Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1287; DB 1; Length 281; 100.0%; Pred. No. 1.6e-97; ive 0; Mismatches 0; Indels 0
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY115578; AAM49797.1; --
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                        32509 MW; DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ol-UCI-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) TMF-related apoptosis inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 TNEMKQLQDNYSKIGLACFSKTDEDFWDSTDGEILNRPCLQVKRQLYQLIEGVTLRTFQD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 TISTVPEKQLSTPPLPRGGRPQKVAAHITGITRRSNSALIPISKDGKTLGQKIESWESSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"Molecular Cloning and Characterization of Chicken Tumor Necrosis
"Molecular Cloning and Characterization of Chicken Tumor Necrosis
Factor (TNP)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
Inducing Ligand (TRAIL).";
J. Vet. Med. Sci. 66:43-650(2004).
EMBL; AB114678; BAC79267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
N-linked (GlcMAc. . .) (Potential).
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor related apoptosis inducing ligand.
                                                                                                                                                                                                                                                                                   MGD; MGI:107414; Thfsf10.
InterPro; IPR006052; TNF family.
InterPro; IPR0060893; TNF_like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF; 1.
PROSITE; PS50049; TNF_2; 1.
Apoptosis; Cytokine; Signal-anchor; Transmembrane.
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66.1%; Pred. No. 1.1e-62;
ive 32; Mismatches 46
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52 52 N
291 AA; 33477 MW;
                                                                                                                                                                                                                     EMBL; U37522; AAC52345.1; -.
HSSP; P50591; 1D2Q.
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Matches 164; Conservative
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Q7T1F2;
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Q7T1F2
              ST FFFFFF SO SERVICE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 NEVKQLQDNYSKIGLACFSKEDGDFWDSTDEGILNRPCLQVKRQLYQLIEEVTLRTFEKT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQE--BIKENTKND-----KQMVQYIYKY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 TSYPDPILLMKSARNSCWSREAEYGLYSIYQGGLFELKENDRIFVSVTNEHLMDLDHEAS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that induces apoptosis.";
Immunity 3:673-682(1995).
-!- FONCTION: Cytokine that binds to TNFRSF10A/TRAILRI,
TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and characterization of a new member of the TNF family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEET
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MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein)
Name=Thfsfl0; Synonyms=Trail;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR003636; TNF_like.
InterPro; IPR003636; TNF_like.
Probom; P000229; TNF; 1.
Probom; P0002012; TNF subf; 1.
PROSITE; PS00251; TNF_li UNKNOWN_1.
PROSITE; PS50049; TNF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: Homotrimer (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein (Potential)
-1- TISSUE SPECIFICITY: Widespread.
-1- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Indels
                                                                                                                                                                                                                                                                                                                                                      287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               68.3%; Score 879; DB 2;
69.7%; Pred. No. 5.2e-64;
ive 25; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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P50592;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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Jones S.J., Marra M.A.;
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MEDINES-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ralusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haideh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bronsfein M.J., Usdin T.B., Toshiyviki S., Carnind P., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny C.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 RISEETISTVQ-EKQQNISPLVRERGPQ----RVAAHITGTRGRSNTLSSPNSKNEKALG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 RKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 DKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 PKQLVQYIYKLTNYPDPILLLMKSARTSCWSKKABYGLYSVYQGGVFQLKREDRIFVSVSN 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 TNELKQLWDTYSRSGTACLTGEELGDLIQNLDVVESKDRVADPCWQVKWHLGKLIKKAMS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TNELKOMODKYSKSGIACFLKEDDSYWDPN----DEESMNSPCWQVKWQLRQLVRKMIL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 HKIHSWESSRRGHSFLYNVELWNGELVVPQTGFYYIYSQTYFRFRENEDEDSGLLERIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                              GO; GO: 0016020; C: membrane; IEA.

GO; GO: 0016020; C: membrane; IEA.

GO; GO: 0005154; F: tumor necrosis factor receptor binding; IEA.

GO; GO: 0006955; P: immune response; IEA.

InterPro; IPR006052; TNF family.

InterPro; IPR008093; TNF like.

InterPro; IPR008093; TNF like.

InterPro; IPR008093; TNF like.

Probom; P000209; TNF 1.

Probom; P000209; TNF 1.

PROSITE; PS00251; TNF 1.

PROSITE; PS00251; TNF 1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 703.5; DB 2; Length 304; 54.7%; Pred. No. 1.4e-49; ive 40; Mismatches 58; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                             34658 MW; DFC128B517747C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Brachydanio rerio (Zebrafish) (Danio rerio)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 EHLIDMDHEASFFGAFLV 242
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273 SDIVDMDKEASFFGAFMI 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             304 AA;
HSSP; P50591; 1D2Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 -----KQMVQYIY-KYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEND 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 SMGESVRGKPMLQYVYKKVSSYQVPILLIMKNARTTCWSRDSEYGLYSIYQAGLFQLGSGD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TSEETISTVQEKQQNISPLV----RERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 SNVLSTWKETFSKSSVSCLMRANLRTIKGQELNGAEGKDDPCWQVTQQLHFLIEKSMSSR 95
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TNELKOMODKYSKSGIACFLKED---DSYWDPNDEESMNSPCWQVKWQLRQLVRK-MILR
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ECO76005; AAH76005.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:tumorn ersponse; IEA.
InterPro; IPR006952; TUP_family.
InterPro; IPR008983; TUP_like.
InterPro; IPR008983; TUP_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.1%; Score 515.5; DB 2; Lengtn .41.7%; Pred. No. 3.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33526 MW; BA776793D2F11ED5 CRC64;
                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 RIFVSVTNEHLIDMDHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||:|:|
273 RVFVTVSNVSTIDMDEKSSFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 299 AA; 33526 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                            sednences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tnfsf10l protein.
Name=tnfsf10l;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                and mouse cDNA
                                                                                                                                                   TISSUE=Whole;
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 DLHQSCRHPVHTW-ANKSFGAHLYNMTLINGRLRVPQDGRYYLYSQVYFRYPSPSDSDQS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 KQTLHAARTRTHSYNTTGSKFMTTV------MQRPSAHLTLSSASDNSRPQSDMHQPQF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRF-QEEIKENT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 ----ILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNT----LSSPNS 103
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TNELKOMODKYSKSGIACFLKEDDSYWDPND-EESMNSPCWOVKWOLROLVRKM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-AB; TISSUE-Whole body;
STRAIN-AB; TISSUE-Whole body;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
R HSSP; PSC951; 1D20.
R ZFIN; ZDB-GENE-010801-1; tnfgf101.
R GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0006955; P: immune response; IEA.
R InterPro; IPR006052; TNF family.
R InterPro; IPR006983; TNF family.
R InterPro; IPR006953; TNF family.
R Probom; PP00209; TNF; 1.
R Probom; PP002012; TNF; subf; 1.
R SMRAT; SW002012; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                               23.9%; Score 307.5; DB 2; Length 317; 29.8%; Pred. No. 5e-17; ive 50; Mismatches 96; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                    317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 TNEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: :: :|:||||
296 SSPTMVYGEDSSSYFGAF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.89
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50049; TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRAIL-like protein.
Name=tnfsf101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 QRVAAHITGTRGRSNT:----LSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGEL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 OSOGSSBELRCLOLINGOGEGSNLEELISNOSC----LKLANTIKAYVATVTENVISRSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 QDKYSKSGIACFLKEDDSYWDPNDEESM-NSPCWQVKWQLRQLVRKMILRTSEETI--ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phaslanidae, Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Indels 28; Gaps
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor receptor binding, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%; Score 305; DB 2; Length 287; 33.7%; Pred. No. 7.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bridgham J.T., Johnson A.L.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AXO57941; AAL23702.1; --
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                ProDom; PD002012; TNF Bubf; 1.
SMART; SM0207; TNF, 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 AA; 32092 MW; DB06E1C95087B108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
TNF-related apoptosis inducing ligand-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.7%; Score 305.5; DB 2; Best Local Similarity 37.6%; Pred. No. 4.4e-17; Matches 62; Conservative 37; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                  F subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00229; TNF; 1.
PRINTS: PROLEZ4; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50049; TNF
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"Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF187319; AAG17031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35370 MW;
                                                                                                      266-318 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Conservative
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620784; Infsf11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199
264
317
318 AA;
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                  VQEKQQ---NISP-LVRERGPQRVAAHI-----TGTRGRSNTLSSPNSKNEKALGR 111
                                                           103 VNEAČKSYFNISEGQVATKTLGKPSÄHLIFRPQNPAQDGSSRRFGNLS------QSCRH 155
                                                                                                      112 KINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQY 171
                                                                                                                                 156 AITRWEDS-TIHSHLQNITYRDGRLRVNQAGKYYVYSQIYFRYSRDGAGARVSVPQLVQC 214
                                                                                                                                                                                               172 IYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMD 231
                                                                                                                                                                                                                      215 INWKTSYSQPILLLKGVGTKCWAPEABYGLHALYQGGLFELKAGDELFVSVSSLAIDYSD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBSEE: 091219;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
59-JUL-2004 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator francear factor lagand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (Osteoclast differentiation factor) (ODF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-TIDIAL Done,
MEDLINE-20540945; PubMed=11092398;
Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIŜSUE=Lung carcinoma;
Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNELKQMQDKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine tumor necrosis factor ligand superfamily member 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kere J.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY312579; AAR16184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 291; DB 2; I
100.0%; Pred. No. 1.4e-16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                     HEASFFGAF 240
                                                                                                                                                                                                                                                                                                                            275 AAASYFGAF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
Name=TNFSF10;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   232
                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                     9 DKYSKSGIACF----LKED----DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSE
                                                                                                                                                                                                                                                   TNFREFILATORY. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         member 11, membrane form.
Tumor necrosis factor ligand superfamily
member 11, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Gaps

    similarity).
    TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
    PTM: The soluble form derives from the membrane form by proteolytic proceesing (By similarity).
    SIMILARITY: Belongs to the tumor necrosis factor family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Homotrimer (By similarity). SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                       Mason-Savas A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Differentiation; Glycoprotein; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%; Score 250.5; DB 1; Length 318; 28.5%; Pred. No. 2.4e-12;
MEDLINE=21662371; PubMed=11804028;
Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Sč
Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein (Potential).
Extracellular (Potential).
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4B87A4D706AD098F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006652; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008363; TNF_like.
Fem; PR00229; TNF, 1.
ProDom; PD02021; TNF, 1.
PROSITE; P800221; TNF gubf; 1.
PROSITE; P800251; TNF 1.
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---GAVQRELQHIV-----GPQRFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADI 176
                                                              PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE 160
                                                                                                                                  232 VPADYLQLAVYVVKTSIKIPSSHNLMKGGSTKAMSGNSEFHFYSINVGGFFKLRAGEEIS 291
                                                                                                                                                                                                                                                               TWIL MOUSE STANDARD; PRT; 316 AA.

035235; 035306; Q9JJK8; Q9JJK9; Q9RLY0;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi Y.;
"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194(1997).
           ETISTVQEKQQNISPLVRERGPQR---VAAHITGT-----RGRS-----NTLSS
                                                                            "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                   161 NTKNDKOMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).

TISSUE=Bone marrow;

MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;

Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,

Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,

Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,

Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Hybridoma;
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
Mong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow stroma;
BEDIINE=B9188248, PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda
                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed=9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                      Name=Tnfsf11; Synonyms=OPGL, RANKL, Trance;
                                                                                                                                                                        242
                                                                                                                                                                                       292 VQVSNPSLLDPDQDATYFGAFKV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Osteoprotegerin ligand is a cytol differentiation ";
                                                                                                                                                                        VSVTNEHLIDMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galibert L.;
                                                                                        177
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                                    126
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1 2.2-A resolution.";
1 July 1 2.2-A resolution.";
2 July 2 2.2-A resolution.";
3 July 1 2.2-A resolution.";
3 July 2 2.2-A resolution.";
3 July 2 2.2-A resolution.";
3 July 2 July 2 July 3 July 3 July 4 July 4 July 5 July 5 July 6 July 7 July 8 J
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Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
"Osteoclast differentiation factor is a ligand for
osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
to TRANCE/RANKL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSIG-035235-3; Sequence-VSP 006448; TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes, but not in nonlymphoid tissues and is abundantly expressed in T cells but not in B cells. A high level expression is also seen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the trabecular bone and lung.

PTM: N-glycosylated.

PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.

DISEASE: Deficiency in Thfsfll results in failure to form lobulo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A., Ueda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
converting enzyme-like protease in shedding of TRANCE, a TNF family
member involved in osteoclastogenesis and dendritic cell survival.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; "Crystal structure of the TRANCE/RANKL cytokine reveals determinants of receptor-ligand specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
"Crystal structure of the extracellular domain of mouse RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21150053; PubMed-11250921; DOI-10.1210/en.142.4.1419; Ikeda T., Kasai M., Utsuyama M., Hirokawa K.; "Determination of three isoforms of the receptor activator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event-Alternative splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=035235-2; Sequence=VSP_006449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISOFORMS 1; 2 AND 3).
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129;
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alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick, irregular growth plates and a relative increase in hypertrophic chondrocytes. SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP_006448.
SSEEMGSGPGVPHEGPLHPAPSAPAPPPPA -> TP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor necrosis factor ligand superfamily member 11, membrane form.

Tumor necrosis factor ligand superfamily member 11, soluble form.
                                                                                                                                                                                                                                                                                                                          EMBL; AF013170; AAC71061.1; -.

REMBL; AF013170; AAC71061.1; -.

REMBL; AF013048; AAB66812.1; -.

REMBL; AB006426; BAA264013.1; -.

REMBL; AB006426; BAA264013.1; -.

REMBL; AB02039; BAA36970.1; -.

REMBL; AB022036; BAA36970.1; JOINED.

REMBL; AB022036; BAA36970.1; JOINED.

REMBL; AB0220377; BAA36970.1; JOINED.

REMBL; AB032771; BAA97259.1; -.

REMBL; AB03777; BAA97259.1; -.

ROG GO:0005515; Proctein binding; IPI.

ROG; GO:00045453; Proctein binding; IPP.

ROG; GO:0004653; Proctein binding; IPP.

ROG; GO:00046570; Proctein binding; IPP.

REPERO; IPR006052; TNF family.

RICEPPO; IPR006052; TNF family.

REPERO; PR006052; TNF family.

REPROSITE; ROGO203; TNF; II.

RESPOND; PR006203; TNF; II.

RESPART; REMBL; RESPOND; REMBL; ARPORTITE; RESPOND; PR006703; TNF; II.

REMBL; AB0377003; TNF; II.

REMBL; AB0377003; TNF; II.

REMBL; AB0377070; TNF; II.

REMBL; AB03770; TNF; II.

REMBL; AB0
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Signal-anchor for type II membrane
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Extracellular (Potential).
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G -> D (in Ref. 2).
Missing (in Ref. 5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 DKOMVOYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 223
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101478; 01423; 026017; 09P203;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
105-JUL-2004 (Rel. 44, Last annotation update)
105-JUL-2004 (Rel. 44, Last annotation update)
106-JUL-2004 (Rel. 40, Last annotation update)
106-JUL-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 DKYSKSGIACF----LKEDDSYWDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEET
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Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUELLY FROM N.A. (ISOFORM 1).

TISSUELLY BURNES BORNES BURNES BORNES BURNES BORNES BURNES 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Obteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; Cell 93:165-176(1998).
                                                                                                                                                                   49;
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TISSUE-Bone marrow, and Peripheral blood;
MEDLINE-98032977; PubMed-9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky B., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
        Length 316;
                                                                                                                                                                   95; Indels
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Ikeda T., Kuroyama H., Hirokawa K.;
"Determination of human RANKL isoforms.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Query Match 18.5%; Score 238.5; DB 1
Best Local Similarity 27.4%; Pred. No. 2.3e-11;
Matches 71; Conservative 44; Mismatches 95
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 NEHLIDMDHEASFFGAFLV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     Isold-014788-3; Sequence=VSP_006446; Isold-014788-3; Sequence=VSP_006446; TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in spleen, peripheral blood Leukocytes, bone marrow, heart, placenta, stemach and thyroid.
INDUCTION: Up-regulated by T cell receptor stimulation. PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing (By similarity). The cleavage may be catalyzed by ADAMIT.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                  "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."; J. Biol. Chem. 272:25190-25194(1997).
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190; Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                               Nagai M., Kyakumoto S., Sato N.;
"Cancer cella responsible for humoral hypercalcemia express mRNA
encoding a secreted form of ODF/TRANCE that induces osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
GO; GO:0000516; F:tumor nesponse; NAS.
GO; GO:003016; P:stecolast differentiation; NAS.
InterPro; IPR006052; TNP_family.
InterPro; IPR008083; TNP_like.
InterPro; IPR00365; TNP_subf.
                                                                                                                     TISSUE=Tongue;
MEDLINE=20175237; Pubmed=10708588; DOI=10.1006/bbrc.2000.2314;
                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2; Synonyme=SODF;
IsoId=014788-2; Sequence=VSP_006447;
                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=014788-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB061227; BAB71768.1; --
BMBL, AB064270; BAB79695.1; --
EMBL, AF013171; AAC51762.1; --
EMBL, AB037599; BAA90488.1; --
GENEW, HGNC:11926; TNFSF11.
                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF019047; AAB86811.1; -. EMBL; AF053712; AAC39731.1; -. EMBL; AB064269; BAB79694.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=3;
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Pfam; PF00229; TNF; 1. ProDom; PD002012; TNF_subf; 1.

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52 KMILRTSEETI----STVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 KALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 QMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 SQHIRAEKAMVDGSWLDLAKRSKLEAQPF------AHLT----INATDIPSGSHK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 DKYSKSGIACF-----LKED----DSYWDPNDEESMNSPCWQVKW------QLRQLVR 51
                                                                                            member 11, membrane form

Tumor necrosis factor ligand superfamily

member 11, soluble form (By similarity).

Cytoplasmic (Potential)

Sjanal-anchor for type II membrane

protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 VSL----SSWYHDR-GWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL
                                                                         Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand."; Cell 76:969-976(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1; Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G., Suda T., Nagata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                Cleavage (By similarity).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
Missing (in isoform 3).
/FIId=VSP 006446.
Missing (In isoform 2).
/FIId=VSP 006447.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
Alternative splicing; Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor; Transmembrane.
CHAIN
CHAIN
Tumor necrosis factor ligand supe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWF6 MOUSE STANDARD; PRT; 279 AA.
P41047; Q61217; Q9R1F2;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                      18.3%; Score 235.5; DB 1; Length 317; 25.3%; Pred. No. 4.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                 766176446348097F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                                                                                                                                                                                                                                                                                                                                                -> G (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Tnfsf6; Synonyms=APT1LG1, Fasl, gld;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 HLIDMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Conservative
                                                                                                            317
                                                                                                                                                                                                                    140
171
198
47
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                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                              140
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CARBOHYD
                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                            VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                DOMAIN
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                                                                                                            CHAIN
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                                                                                                                                                                                                                         SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity.";

Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).

1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.

TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).
                                                                                                                                           MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6; Lynch D.H., Watebon M.L., Alderson M.R., Baum P.R., Miller R.E., Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic processing (By similarity).

By Adeficiency in this protein is the cause of generalized lymphoproliferation disease phenotype (gld). Gld mice present lymphodenopathy and autoantibody production. The phenotype is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.
                     Pettsch M.J., Tschopp J.J.;
"Comparative molecular modelling of the Fas-ligand and other members
of the TMF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20021694; PubMed=10552956; Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R., Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R., Comnarile L., Migliorati G., Delfino D.V., Riccardi C.; "Cloning and expression of a short Fas ligand: a new alternatively spliced product of the mouse Fas ligand gene."; Blood 94:3456-3467(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS ALA-184 AND GLY-218.
STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
                                                                                                                                                                                                                                                                                                                                     Fenner M.H., Shioda T., Isselbacher K.J.; "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF VARIANT GLD.
MEDLINE=96091792; PubMed=7495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rousseau M., Bron C., Renno T., French L., Tschopp J.;
"Characterization of the non-functional Fas ligand of gld mice.";
Int. Immunol. 7:1381-1386(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism of murine Fas ligand that affects the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recessively inherited. SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=P41047-2; Sequence=VSP 006445;
PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P41047-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted (isoforms FASL and FASLS).
                                                                                                                                                                                                                                                                                                                                                                                                                          [5]
SEQUENCE FROM N.A. (ISOFORM FASLS)
                                                                                                    [3]
SEQUENCE FROM N.A. (ISOFORM FASL).
                                                                                                                                                                                                                                                                            [4]
SEQUENCE FROM N.A. (ISOFORM FASL).
                                                                              Mol. Immunol. 32:761-772(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C3H; TISSUE=Spleen;
                                                                                                                                                                                                                                                    [mmunity 1:131-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS
                                                             family.";
                                                                                                                                                                                                                                gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=FasLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=FasL;
                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                   amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /agita H.
                                                                                                                                                                                                                                   Eamily
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch). 202 NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI 259 45 OLROLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK 104 111 BLREFTNOSL------KVSSFEKOIANPSTPSEKKEPRSV-AHLTG------NPHSR 154 105 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN 164 Missing (in isoform FasLS).

/FIId=VSP_006445.

T -> A (in strain BALB/c, strain DBA/1
and strain DBA/2; enhances cytotoxicity).
E -> G (in strain BALB/c, strain DBA/1
and strain DBA/2; enhances cytotoxicity).
F -> L (in gld; abolishes binding of FASL PRINTS; PRO1681;
PRINTS; PRO1681;
PRINTS; PRO1234; TNECROSIS;
PRODOM; PD002012; TNF subf; 1.
PROSITE; PS0049; TNF 1; 1.
PROSITE; PS0049; TNF 2; 1.
Alternative splicing; Apoptosis, Cytokine; Disease mutation;
Alternative splicing; Apoptosis, Cytokine; Apoptosis, Cytokin 165 DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 33; Gaps N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential) Signal-anchor for type II membrane 14.7%; Score 189.5; DB 1; Length 279; 25.8%; Pred. No. 2.1e-07; tive 50; Mismatches 64; Indels 33 Cleavage (By similarity). Potential. 37972E2728E0A1CA CRC64; protein (Potential). Extracellular (Potential) to its recep Poly-Pro. Pro-rich. HSSP; P50591; 1DG6.
MGD; MG1:99255; Tnfsf6.
InterPro; IPR006063; TNF abc.
InterPro; IPR006053; TNF abc.
InterPro; IPR00652; TNF family.
InterPro; IPR008981; TNF family.
InterPro; IPR008981; TNF subf.
Pfam; PF00229; TNF; 1. 223 INEHLIDMDHEASFFGAF 240 : ||: : :|| : 260 SQLSLINFEESKTFFGLY 277 EMBL, U06948; AAA17800.1; -EMBL, U10994; AAA1778.1; -EMBL, S76752; AAB3780.1; -EMBL, U58995; AAB02915.1; -EMBL, AFL19335; AAB02915.1; -PIR; A53062; A33062. 279 AA; 31442 MW; 51; Conservative 279 69 51 128 231 117 78 Query Match Best Local Similarity 218 273 184 101 SEQUENCE TRANSMEM DISULFID CARBOHYD CARBOHYD CARBOHYD /ARSPLIC CARBOHYD /ARIANT /ARIANT **JARIANT** DOMAIN DOMAIN DOMAIN Matches g à 엄 ò 셤 ò two MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;

9

us-10-662-429-2_copy_39_281.rup

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and mouse
                      CARBOHYD
CARBOHYD
    CARBOHYD
                                                             SEQUENCE
                                                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                       Prodom, co. SMART; 1.

PROSITE; PS00251; TNF 1; 1.

PROSITE; PS50049; TNF 2; 1.

Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.

Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.

CHAIN 129 280 Tumor necrosis factor ligand superfamily member 6, member 6 octobe form. (By similarity).

DOMAIN 1 80 Cytoplasmic (Potential).

TRANSMEM 81 101 Signal-anchor for type II membrane protein (Potential).
                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
                                                                                                                                                      (CD95L protein).
Name=TNFSFG, Synonyms=CD95L, FASL;
Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey)
Bukaryota; Metazoa; Choordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                    TISSUE=Lymphocytes;
MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.
"Cloning, sequencing, and homology analysis of nonhuman primat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteclytic processing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly-Pro.
Cleavage (By similarity).
                                        280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008064; Fas_ligand.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR00836; TNF_like.
IPfam; PF00229; TNF; 1.
PRINTS; PR01881; FASLIGAND.
PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF_subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF344847; AAK37606.1; -.
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                        Cercopithecinae; Cercocebus.
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280
69
64
129
232
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
128
201
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                                      TNF6
RESULT 14
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=57BL/GNCT; TISSUB=Hematopoietic Stem Cell;

STRAIN=237BL/GNCT; TISSUB=Hematopoietic Stem Cell;

STRAIN=233B6257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

RA STRAINS=23B6257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

RA STRAINS=28 E., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechui S.F., Zeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altechui S.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

Bothert S.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.A., Nochey K.C., Hale S., Carninci P., Prange C.,

RA Bosak S.A., MocWan D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Grimmood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RAZywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.;

RA Gerenation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                          44 WQLRQLVRKMI-LR--TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSS 100
                                                                                                                                                                                                                                                                                                                                  101 PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 NTKNDKQMVQYIY-KYTSYPDPILLLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 -SCINLPLSHKVYMRNSKYPQDLVVMBGKOMS-YCITGQMWAHSSYLGAVFNLTSTDHLY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 PNSRSMPL-----EWEDT-YGIVLLSGVKYKKGGLVINETGLYPVYSKVYPRGQ----
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
   1-linked (GlcNAc. .) (Potential)
1-linked (GlcNAc. .) (Potential)
1-linked (GlcNAc. .) (Potential)
729EA60067B7D398 CRC64;
                                                                                                                                                          14.4%; Score 185.5; DB 1; Length 280; 27.4%; Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; F50591; IDG6.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0046666; P:retinal programmed cell death; IMP.
InterPro; IPR006052; TNF Emmily.
InterPro; IPR008983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                        177;
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                                                                                                                                                                                                                               42; Mismatches
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N-linked
N-linked
N-linked
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                                                                                                  31407 MW;
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                                                                                                                                                                                              Local Similarity 27.49 tes 55; Conservative
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   183
249
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280 AA;
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Search completed: June 22, 2005, 06:01:10 Job time : 101.168 secs

260 SQLSLINFEESKTFFGLY 277

Human Apo
Human Apo
Human neo
Human TRA

Abg 73861
Abu10205
Abu10205
Abu10205
Abu10205
Abg 72738
Abg 72738
Abg 72139
Abg 7305
Abg 7306

Human Human Human

Human Human Human

OM protein

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Run

Sequence:

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TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation; arthritis; septicaemia; transplant rejection; autoimmune disease; inflammatory bowel disease; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; psoriasis; restenosis; brain injury; AIDS; bone disease; cancer; atherosclerosis; Alzheimer's disease; human; therapy; diagnosis; ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of human TL2 (also known as TRAIL), which has newly been discovered to be a ligand of human tumour necrosis related receptor TR5 (see AAW7631). This TR5 polypeptide of the invention and TL2 can be used in screening processes for compounds which bind the receptor, or its ligand, and which activate (agonists) or inhibit (ancagonists) the receptor or TL2. Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide encoding TRS polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury, AIDS and bone diseases.
                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truneh A, Lyn SDP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 17-18; 22pp; English.
                 ABU71443
ABG72738
AAO29543
ABU08558
                                                       ABR42313
ABG71905
ABG71905
AAB360546
AAB31151
ABO25125
ADB1471
ADD14080
ADD14080
ABD14080
ABD14080
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ADK72311
                                                                                                                                                                                ADK72303
                                                                                                                                                                                                                                                           AAW76332 standard; protein; 279 AA
                                                                                                                                                                                                                                                                                                                  Human TL2 (TRAIL), ligand for TR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP
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97US-00901469
                                                                                                                                                                                                                                                                                                (first entry)
WPI; 1998-497862/43.
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Ношо варіеня
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Protein a Human Apo Human Apo Human PRO Amino aci Human PRO Human PRO Human TNF Human TNF Human TRA Human Apo
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Human Apo
Human apo
Human TL2
Human TRA
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Aaw95032 Tumour ne
                                                               June 22, 2005, 05:57:23 ; Search time 108.052 Seconds (without alignments) 869.796 Million cell updates/sec
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                                                                                                                       TNELKQMQDKYSKSGIACFL.....NEHLIDMDHEASFFGAFLVG 243
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Aab67243
Aae11031
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Abb08133
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Aay27012
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                      2105692 segs, 386760381 residues
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                                              - protein search, using sw model
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AAW56760
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geneseqp1990s:*
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geneseqp2001s:*
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Minimum Maximum

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Human Apo C neoform Human TNF

Aao19095 Aau79593

ABP51954 AA019095 AAU79593

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            expression of the nuclectide sequence encoding the polypeptide and/or administering a polypeptide that competes with the polypeptide for its ligand, substrate or receptor. The active agents can be used for the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease
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                                                                                                                                                                                                                                                                                         TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
                                                                                                                                                                                                                                                         Gaps
the polypeptide, administering a nucleic acid that inhibits the
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                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                     100.0%; Score 1287; DB 2; Length 279; 100.0%; Pred. No. 3.4e-117; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95032 standard; protein; 279 AA.
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97US-0056980P.
97US-0057550P.
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 243; Conservative
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                                                                                                                                                                                       Sequence 279 AA;
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Identifying agonists and antagonists to tumour necrosis factor receptor

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The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method compirates: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2 or TL4 with a candidate compound in the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, inflection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, athersclerosis and Alzabiner's disease. The present sequence represents a TNF-R related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180
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(TNF-R) related polypeptides (LR1, LR2, LT2 and LT4) - useful for
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1287; DB 2; Length 279; 100.0%; Pred. No. 3.4e-117; ive 0; Mismatches 0; Indels 0
               treating stroke, Alzheimer's disease and AIDS
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/label= Transmembrane_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .14
/label= Cytoplasmic_region
                                               Disclosure; Page 14-15; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW19777 standard; protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41. .281
/note= "Claim 2"
41. .281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15. .281
/note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel cytokine Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
Les 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .281
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 LVG 279
                                                                                                                                                                                                                                                                                                                             Sequence 279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LVG 243
                                                                                                                                                                                                                                                                                          polypeptide TL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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Human Apoptosis inducing molecule-I (AIM-I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVG 281
                                                                                      WO9733899-A1.
                                                                                                                                 14-MAR-1996;
                                                                 Homo sapiens
                                                                                                           18-SEP-1997
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                                                                                                                                                                                                                                                                                            A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILLMKSARNSCWSKDAEYGLYSIYQGGIFBLKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISTVOEKOONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGHSFLSNLHLRNGELVIHEKGFYYIXSQTYFRPQEEIKENTKNDKQWVQYIYKYTSYPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                       Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce apoptosis for the treatment of breast and colon cancer.
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                   /label= Glycosylation
/note= "putative N-linked glycosylation site"
/lote= "Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1287; DB 2; Length 281; 100.0%; Pred. No. 3.4e-117;
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/label= Extracellular_region
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                                                                                                                                                                                      Kim KJ;
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                                                                                                                                                                                    Ashkenazi AJ, Chuntharapai A,
                                                                                                                                                                                                                                                                          Claim 4; Fig 1a; 72pp; English
                                                                                                                     97WO-US000272
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Matches 243; Conservative
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                                                                                                                                                                                                                     N-PSDB; AAT72796
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 281 AA;
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            Modified-site
                                                                                                                     08-JAN-1997;
                                                                                                                                           09-JAN-1996;
                                                                          WO9725428-A1
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                                                                                                17-JUL-1997.
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                                            Protein
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ID AAW2
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AC AAW2
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The present sequence represents a human Apoptosis inducing molecule-I (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand superfamily. The products can be used in the diagnosis and treatment of disorders related to under-expression, over-expression or altered expression of AIM-I. AIM-I or agonists can be used for treating autoimmunoproliferative disease lymphadenopathy (IPL), rheumatosus, immunoproliferative lymphadenopathy (ILL), rheumatoid arthritis, diabetes, and multiple sclerosis, graft versus host disease, to inhibit neoplasis such as tumour cell growth, to treat restrenosis, to regulate neoplasis in endothelial cell development, to stimulate peripheral colerance and cytotoxic T-cell mediated apoptosis. Antagonists can be used for treating cachexia, cerebral malaria, rheumatoid arthritis or osteoporosis, for preventing graft-host rejection, and as anti-illammatory agents, for treating endotoxic shock or to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated apoptosis inducing molecule-I - used to develop products for the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft versus host disease or inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Apoptosis inducing molecule-I; AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily; AIM-I altered expression; neoplasia inhibition; anti-inflammatory agent.
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100.0%; Pred. No. 3.4e-117;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 1; 82pp; English.
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Matches 243; Conservative
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120

180 218 240

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61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAM19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AA772848), deposited in vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral infection and for use in assays.
                                                                                                                                                                                                                                                                                                                                      /note= "potential KEX2 protease processing site"
109. .111
/note= "potential N-glycosylation site"
149. .150
                                                                                                                                  Tumour necrosis factor related apoptosis inducing ligand; TRAIL; cytokine; cancer; leukaemia; lyphoma; melanoma; viral infection; thrombotic microangloplasty; therapy.
                                                                                                                                                                                                                                                                                                                                                                                           /note= "potential KEX2 protease processing site"
                                                                                                                                                                                                                                                                                  39. .281
/label= Extracelular_domain
/note= "contains a receptor-binding region"
                                                                                                                                                                                                                  1. .18
/label= Cytoplasmic_domain
19. .38
/label= Transmembrane_domain
39. .281
                                                                                                         Human apoptosis inducer cytokine TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 43-44; 62pp; English
                          AAW19787 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00496632
95US-00548368
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV) IMMUNEX CORP.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Cleavage-site
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
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                                                                               24-SEP-1997
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       WO9701633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SR,
                                                     AAW19787;
                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                   Domain
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RESULT 5
AAW19787
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This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in polyabetion of the novel human TNF related receptor, TR6. TR6 polyapetides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriaeis), transplant rejection, graft vs. host disease, inflammation, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) ALDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease
99 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                                                                                                      219 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation, arthritis, septicaemia, autoimmune disease, restenosis, transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis, Alzheimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour necrosis factor related receptor; human; treatment; stroke;
                                                                           159 SGHSFLSNLHLRNGELVIHEKGFYYIXSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
                                                     SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
                                                                                                                                    PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide, antibody, agonist, antagonist, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 32-33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                      AAW76829 standard; protein; 281 AA.
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97US-00916625.
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N-PSDB; AAV63096.
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                                                                                                                                                                                                                241 LVG 243
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22-AUG-1997;
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Length 281;

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                                                                                                                                                                                                                                                                                                                                                                                          SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180
    studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections
                                                                                                                                                                                                                                                 39 TNELKQMQDKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
                                                                                                                                                                                                                                                                                                                                                                                                                 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
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0; Mismatches 0;
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                                                                                                                                            100.0%;
llarity 100.0%;
Conservative 0
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                                                                                                                                            Query Match
Best Local Similarity
Matches 243; Conserv
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                                                                                                       Sequence 281 AA;
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                                                            TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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  100.0%; Pred. No. 3.4e-117; ive 0; Mismatches 0;
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95US-00548368
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39. .281
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N-PSDB; AAV29518.
Best Local Similarity
Matches 243; Conserv
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01-NOV-1995;
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The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF) related protein, involved in inflammation, myelopoiesis and bene resorption. It has the same nucleic acid and maino acid (as) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
                                                                                               Human, AGP-1, tumour necrosis factor-related protein, TNF, inflammation, bone resorption; haematopoietic disease.
                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein - useful for treating inflammation, bone resorption and haematopoietic
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reagents for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid archirits, systemic lupus erythematosus, psoriasis, scleroderma, infection-related inflammation) or bone resorption diseases (e.g. osteoporosis, osteomyolitis, hypercalcaemia, Paget's disease). AGP-1 can be used to treat haematopoietic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to
                                                                                                                                                                                                                                                                                                                                                                                 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; surface receptor; TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein associated with neurodegenerative and autoimmune diseases
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                                                                                                                                                                                                                                           100.0%; Score 1287; DB 2; Length 281; 100.0%; Pred. No. 3.4e-117; ive 0, Mismatches 0; Indels 0
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 243; Conservative
                                                                                                                                                                              produce recombinant AGP-1
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                                      The specification describes the use a polypeptide corresponding to at dieast the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory disease. The polypeptides can be used in treatment of neurodegenerative disease. The polypeptides can rhumematorid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and anti-TRAIL antibody or a TRAIL equivalent that binds to specific an receptors, inhibiting formation of natural complex
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100.0%; Pred. No. 3.4e-117;
iive 0; Mismatches 0;
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               Claim 2; Page 13; 21pp; French.
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N-PSDB; AAX86987.
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15-APR-1998;
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                                                                    This sequence represents a novel human cytokine, designated Apo-2 ligand (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant methodology. Apo-2L is useful for inducing apoprosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immunemediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases
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designated Apo-2 ligand, useful for inducing apoptosis
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                                                                                                                                                                                                          associated with increased apoptosis
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                                          Claim 1; Fig 1A; 86pp; English
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                mammalian cancer cells
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New isolated monoclonal antibodies having antigen specificity for Apo-2 ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo-2 ligand serum, and for treating diseases associated with increased
                                                                                                                     This sequence is the human Apo-2 ligand protein, which is recognised by monoclonal antibodies produced by the hybridoma cell lines of the invention. The hybridoma cell lines are deposited under the American Type Culture Collection Accession Numbers: ATCC HB-1255, HB-12257, HB-12258 and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic assays for Apo-2 ligand, e.g. detecting its expression in specific cells, tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand antibodies associated with increased apoptosis. They are also useful for the affinity purification of Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells
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identification; tumourigenesis; anticancer; detection.
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Pred. No. 3.4e-117;
0; Mismatches 0;
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                                                                                        Claim 9; Fig la; 46pp; English
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99US-0162506P.
99WO-US028313.
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Matches 243; Conservative
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29-OCT-1999;
30-NOV-1999;
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                                                        apoptosis.
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The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
                                                                                                                                                                                                                             Killing of tumor cells, e.g. solid tumors or carcinoma, comprises administration of synergistic combination of diterpenoid diepoxide and tumor necrosis factor related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                  Disclosure; Page 23-24; 29pp; English.
                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR
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                                                                                     LS-FEB-2000; 2000WO-US003891.
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                                                                                                                                                                                           WPI; 2000-558253/51.
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                                    WO200048619-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           lung carcinoma
             Homo sapiens.
                                                                                                              16-FEB-1999;
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                                                                                                                                                                                           present invention describes an antibody that binds to a human protein
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                                                                                                              Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression.
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                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide; TTNF related apoptosis-inducing ligand; tumour cell; TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma; non-small cell lung carcinoma.
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                                                 Watanabe CK,
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                                                 Roy MA,
                                                 Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08545 standard; protein; 281 AA.
                                                                                                                                                                 Claim 61; Fig 36; 226pp; English.
99WO-US028634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                 Goddard A,
                        (GETH ) GENENTECH INC
                                                                          2000-594320/56
                                                                         WPI; 2000-594320/
N-PSDB; AAC58120.
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01-DEC-1999;
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99 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
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                                                                                                                                                                                                                                TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
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                                                                                                                 1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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                                                              Gaps
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  Length 281;
                                                        Indels
100.0%; Score 1287; DB 3;
100.0%; Pred. No. 3.4e-117;
tive 0; Mismatches 0;
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(first entry)

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Human, PRO; cytostatic; nootropic; neuroprotective; respiratory general;
antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.
                         Human PRO1096 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                         WO200073348-A2.
                                                                                                                                                                         30-MAY-2000;
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 21-MAR-2001
                                                                                                                                                07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP,
 The present sequence is human AGP-1, a type II transmembrane protein. Version proteins comprising an FC immunoglobulin region fused to the Neterminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1
antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis.
                                                                                                                                                                                                                                                                      Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 281;
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100.0%; Pred. No. 3.4e-117;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins used in prior art therapies
                                                                                                                                                                                                                                                                                                            Claim 3; Fig 2; 93pp; English
                                                                                                                                                            99US-00293245
                                                                                                                                   24-MAR-2000; 2000WO-US008004
                                                                                                                                                                                                                                   WPI; 2000-665240/64.
N-PSDB; AAC67831.
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                                                                                                                                                                                    (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281 AA;
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                                                                                    WO200063253-A1
                                                             Homo sapiens
                                                                                                                                                            16-APR-1999;
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Matches
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99WO-US012252. 99US-0140650P. 99US-0141037P. 99US-0144758P. 99WO-US020111.

99WO-US020594 99US-0162506P

99WO-US028551. 99US-0170262P. 99WO-US030095. 99WO-US028313. 99WO-US028634.

2000WO-US004341. 2000WO-US005841.

2000US-0187202P 2000WO-US006319 2000WO-US006884 2000WO-US013705

2000WO-US000376

99WO-US030999 2000WO-US003565 2000WO-US004342

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Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
                                                                                                                                                                                                                                                                                                                 The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prosetac cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastoccelic disorders, and inflammatory, angiogenic and immunological
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100.0%; Score 1287; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.4e-117;
Matches 243; Conservative 0; Mismatches 0;
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WPI; 2001-016509/02.
                                  N-PSDB; AAC91579
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Goddard A, Smith V,

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AAB50977 standard; protein; 281 AA

RESULT 15

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3: /cgn2_6/ptodata/2/pubpaa/NSO6_NBW_PUB_pep:*
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6: /cgn2_6/ptodata/2/pubpaa/NSO7_NBW_PUB_pep:*
7: /cgn2_6/ptodata/2/pubpaa/NSO8_NBW_PUB_pep:*
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                                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Query Match 100.0%; Score 1287; DB 13; Length 279; Best Local Similarity 100.0%; Pred. No. 1e-110; Matches 243; Conservative 0; Mismatches 0; Indels 0;

Sequence 21, Appl Sequence 20, Appl Sequence 20, Appl Sequence 66, Appl Sequence 66, Appl Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2,	G AGONIST AND NECROSIS RELATED RECEPTORS TR1 AND TR2
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44444000000000000000000000000000000000	US/100662 1151110A1 ke, Michae er R. MRETHON DF 30-D1 MBER: US/1 20-110-25 ER: 60/055 ER: 60/055 ER: 60/056 ER: 60/056 ER: 60/056 FR: 60/056 FR: 60/057 7-08-29 Windows Ve
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71110000000000000000000000000000000000	Application Mo. US200201 NMA. US200201 NMA. US200201 NMATION: Brigham-Burk Young, Pete Young, Pete YOUNG, Pate YOUNG, Pete YOU
1287 1287 1287 1287 1287 1287 1287 1287	0 -209- 1 -209- 1 -200 - 1 -209- 1 -209-
	RESULT 1 US-10-066; Sequence; Publicat GENERAL APPLICATION TITLE COURREN COURREN COURREN PRIOR 1 PRIOR

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99 TISTVQEKQONISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                                                                                        219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
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39 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWOVKWQLRQLVRKMILRTSEE 98
                                                                                                                       SGHSFLSNLHLRNGELVIHEKGFYYIYSOTYFRFOEEIKENTKNDKOMVOYIYKYTSYPD
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                                        61 TISTVOEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR
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100.0%; Pred. No. 1e-110;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08971317A
Publication No. US20010010925A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWF-DELTA LIGAND AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A FILING DATE: 17-NOV-1997
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STREET: 100 Abbott Park Road
CITY: Abbott Park
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimi C
REGISTRATION NUMBER: 39, (
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SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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Matches 243; Conservative
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COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Con
OPERATING SYSTEM:
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TELEFAX: (
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                                                                                                                                                                                                       PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                                                                                                                               217 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
                                                                              97 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
                                                                                                                       SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
37 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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; Publication No. US20010010924A1
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
ITLE OF INVENTION: RECEPTOR, TR6
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: AFAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 100.0%; Score 1287; DB 8; al Similarity 100.0%; Pred. No. 1e-110; 243; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOCTWARE: FASELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,625B
FILING DATE: 22-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/853,684
FILING DATE: 14-MARCH-1997
APPLICATION NUMBER: 60/041,230
FILING DATE: 14-MARCH-1997
ATYORNEY/AGENT INFORMATION:
NAME: PRESTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50008-1
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TELECOMULNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEFAX: 846169
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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Best Local Similarity
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US-08-916-625B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 SGHSFLSNLHLRNGELVIHEKGPYYIXSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
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                                                                                                                                                                                                                                                                    1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
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                                                                                                                                                                               Query Match 100.0%; Score 1287; DB 9; Best Local Similarity 100.0%; Pred. No. 1e-110; Matches 243; Conservative 0; Mismatches 0;
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Sequence 1, Application US/09934465
Sequence 1, USZ0020102233A1
GENERAL INFORMATION:
APPLICANT: ABARENAZI, AVI J.
TITLE OF INVERTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
; EARLIER FILING DATE: 1997-11-17; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PR
ORGANISM: Home sapiens
US-09-193-663-8
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APPLICANT: Bristol-Myers Suibb Company
APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION WHOBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
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                                                             SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
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Patent No. US20020055624A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
FILE REFERENCE: 6255.US.02
CURRENT APPLICATION UNMER: US/09/193,663
CURRENT APPLICATION NUMBER: 60/065,916
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; Patent No. US20020012968A1
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Matches 243; Conservative
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US-09-813-329-17
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LENGTH: 281.
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US-09-193-663-8
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61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
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                                                                                                    1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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100.0%; Score 1287; DB 13; Length 281; 100.0%; Pred. No. 1e-110; ive 0; Mismatches 0; Indels 0;
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CURRENT PILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/05914
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07980
PRIOR PILING DATE: 1998-04-24
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-08-17
PRIOR PLING DATE: 1998-08-17
PRIOR PLING DATE: 1998-08-17
PRIOR PLING DATE: 1998-08-17
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
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Query Match
Best Local Similarity 100.
Matches 243; Conservative
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Hebert, Carolyn
Henzel, William
Kabakoff, Rhona
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Smith, Victoria
Watanabe, Colin
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Goddard, Audrey
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Publication No. US20030108871A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 118
LENGTH: 281
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OTHER INFORMATĪON: Incyte ID No. US20030108871A1 059509CD1
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; Publication No. US200201423881
; GENERAL INFORMATION; APPLICANT: CHEN, Christina Yu-Ching; TTLE OF INVENTION: BACTERIAL HOST STRAINS; TILE REFERENCE: P1804R1
; CURRENT APPLICATION UNMBER: US/10/011,125; CURRENT FILING DATE: 2001-12-07; PRIOR APPLICATION NUMBER: US 60/256,162; PRIOR FILING DATE: 2000-12-14; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4; SEQ ID NOS: 10
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Matches 243; Conservative
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; ORGANISM: Homo sapiens
US-10-011-125-4
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ORGANISM: Homo sapiens
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279 LVG 281
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US-09-919-039-118
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US-10-011-125-4
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PRIOR APPLICATION NUMBER: 607-15
PRIOR APPLICATION NUMBER: 607-131
PRIOR APPLICATION NUMBER: 607-131
PRIOR APPLICATION NUMBER: 607-132
PRIOR PAPLICATION NUMBER: 607-136
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99 IISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 49001

COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 Diskette
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                     APPLICANT: Bienkowski, Michael J
Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1287; DB 1-
100.0%; Pred. No. 1e-110;
ative 0; Mismatches 0
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REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Legal Services
                                                                                                                                                                                     Sequence 11, Application US/10174654 Publication No. US20030044937A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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STATE: MI
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US-10-174-654-11
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Best Local S
Matches 243
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Publication No. US20030013099A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
APPLICANT: Gones, David A.
APPLICANT: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT APPLICATION NUMBER: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL PROGRAM
SEQ ID NO 54
LENGTH: 281
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                                                                                                                                      Query Match 100.0%; Score 1287; DB 13; Length 281; Best Local Similarity 100.0%; Pred. No. 1e-110; Matches 243; Conservative 0; Mismatches 0; Indels 0;
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OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
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Matches 243; Conservative
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                 LENGTH: 281
TYPE: PRT
ORGANISM: Homo Sapien
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US-10-093-766-54
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i Sequence 7.2. Application US/10322673

j Sequence 7.2. Application US/10322673

j Fublication No. US20030180296A1

j GENERAL INFORMATION:

j APPLICATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PFS85

CURRENT APPLICATION NUMBER: US/10/322,673

CURRENT FILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/384,828

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 72

LENGTH: 281
                                                                           39 TNELKQMQDKYSKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
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100.0%; Pred. No. 1e-110;
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Best Local Similarity 100.0
Matches 243; Conservative
    Conservative
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; ORGANISM: Homo sapiens
US-10-322-673-72
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; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
    APPLICANT: Human Genome Sciences, Inc.
    TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
    TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
    TITLE OF INVENTION: Human Endokine Alpha
    FILE REFERENCE: PF561
    CURRENT PILING DATE: 2002-08-15
    PRIOR PLILING DATE: 2001-08-16
    PRIOR PLILING DATE: 2001-10-30
    NUMBER OF SEQ ID NOS: 57
    SEQ ID NOS: 57
    SEQ ID NO 20
    LENTHH: 281

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                                                                                                     Sequence 41, Application US/10151882
| Publication No. US20030059862A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
| TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
| TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
| CURRENT APPLICATION NUMBER: US/10/151,882
| CURRENT FILING DATE: 2002-05-22
| PRIOR APPLICATION NUMBER: 60/293,100
| PRIOR APPLICATION NUMBER: 60/293,100
| PRIOR PILING DATE: 2001-05-24
| NUMBER OF SEQ ID NOS: 48
| SSOTTWARE: Patentin version 3.0
| SSOTTWARE: 281
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Pred. No. 1e-110;
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100.0%;
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; ORGANISM: Homo sapiens
US-10-151-882-41
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Best Local Similarity
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CRGANISM: human
US-10-218-547-20
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US-10-218-547-20
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241 LVG 243

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RESULT 15
US-10-139-785-66

i Sequence 66, Application US/10139785

j Publication No. UG20030190685A1

i GENERAL INFORMATION:

i TTILE OF INVENTION: Attribodies that Immunospecifically Bind to TRAIL

i TTILE OF INVENTION: Receptors

f TILE OF INVENTION: Receptors

f TILE OF INVENTION: Receptors

i TTILE OF INVENTION: Receptors

f TILE OF INVENTION: DATE: 2002-05-07

CURRENT PELING DATE: 2002-04-06

pRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR APPLICATION NUMBER: 60/331,044

PRIOR FILING DATE: 2001-11-17

PRIOR FILING DATE: 2001-10-7

PRIOR PELING DATE: 2001-10-8

PRIOR PELING DATE: 2001-09-21

PRIOR PELING DATE: 2001-09-21

PRIOR PELING DATE: 2001-09-22

PRIOR PELING DATE: 2001-09-22

PRIOR PELING DATE: 2001-09-22

PRIOR PELING DATE: 2001-09-22

PRIOR PELING DATE: 2001-08-02

PRIOR PELING DATE: 2001-08-03

PRIOR PELING DATE
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CRGANISM: Homo sapiens
US-10-139-785-66
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279 LVG 281
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SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 218 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240 61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120 121 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180 39 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 98 1 TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE Gaps ö 181 159 셤 g ð ò a ò

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219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278 LVG 243 279 LVG 281 241 ద ઠે

Search completed: June 22, 2005, 06:39:14 Job time : 565.372 secs

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157 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRPQEEIKENTKNDKQMVQYIYKYTSYPD 216
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Sequence 10
Sequence 2,
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Sequence 12, Appl Sequence 32, Appl Sequence 34, Appli Sequence 4, Appli Sequence 4, Appli Sequence 13, Appli Sequence 11, Appl	AND RELATED RECEPTORS TR1 AND TR2	Length 279; Indels 0; Gaps 0; MQVKWQLRQLVRKMILRTSEE 60
4 US-09-632-287A-12 4 US-09-513-999C-7833 4 US-09-569-611C-32 1 US-08-670-328-4 4 US-09-320-424-4 4 US-09-825-563-4 5 PCT-USS-10855-4 4 US-09-825-563-4 6 US-09-825-563-4 7 US-09-825-11 8 US-09-632-287A-13 9 US-09-957-800-11 4 US-09-577-800-11 4 US-09-871-865-11 4 US-09-871-865-11 4 US-09-871-856-11 4 US-09-871-856-11	ALIGNMENTS n. US/09072993C Brigham-Burke Young NETHOD OF IDENTIFYING AGONIST ANTAGONISTS FOR TUMOR NECROSIS 030 0130 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-06-09 197-08-19 197-08-29 197-08-29 197-08-29 197-08-29 197-08-29	Score 1287; DB 3; Pred: No. 2:8e-125; O; Mismatches O; CLEDDSYWDPNDEESMNSPC CLEDDSYWDPNDEESMNSPC CLEDDSYWDPNDEESMNSPC CLEDDSYWDPNDEESMNSPC CLEDDSYWDPNDEESMNSPC CLEDDSYWDPNDEESMNSPC CLEDDSYWDPNDEESMNSPC CLEDDSYNAHITGTRGRSNTLS CLEDDSYNAHITGTRGRSNTLS CLEDDSYYTYSQTYFRFQBEIK CLEDDSYMDPH CLEDDSYMDP
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COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 incl
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; ORGANISM: Homo sapiens
US-08-584-031-1
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Best Local Similarity
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                                                 Sequence 2, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCE: Kathiryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                     STATE: "...

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-UUW-1996
CLASSIFICATION: 435
FRIOR APPLICATION: 435
FILING DATE: 29-UUN-1995
CLASSIFICATION: 435
FILING DATE: 29-UUN-1995
CLASSIFICATION: 435
FILING DATE: 10-UOV-1995
CLASSIFICATION: 435
FILING DATE: 01-UOV-1995
CLASSIFICATION: 435
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
FILING DATE: 29-UN-1995
CLASSIFICATION: 435
FILING DATE: 29-UN-1995
CLASSIFICATION: 435
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
FILING DATE: 29-UN-1995
CLASSIFICATION: 435
FILING DATE: 2835-B
TELECOMMUNICATION INFORMATION:
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TELEK: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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RESULT 2
US-08-670-354-2
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Fatent No. 6046048
Fatent No. 6046048
FAPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim TITLE OF INVENTION:
FAPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim TITLE OF INVENTION:
FAPLICANT: Apple Sequences: 8
CORRESPONDENCES: 8
CORRESPONDENCES: Benemech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STATE: California
COUNTRY: USA
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100.0%; Pred. No. 2.9e-125;
ive 0; Mismatches 0;
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RESULT 3
US-08-584-031-1
Sequence 1, Application US/08584031A
Fatent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
FILE REFERENCE: 11669-22USO3
CURRENT PELING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOOTWARE PATENT PLING PATE: 1996-01-09
SEQ ID NO 1
LENGTH: 281
LENGTH: 281
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61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
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                                                                                                                                                                                                                                 Indels
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TITLE OF INVENTION: CYtokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION CYTOKINE that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER PILING DATE: 1998-01-10
EARLIER PELICATION NUMBER: 09/190,046
EARLIER PILING DATE: 1998-03-26
EARLIER PILING DATE: 1998-03-26
EARLIER PILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1995-06-29
EARLIER PELING DATE: 1995-06-29
NUMBER: OF SEQ ID NOS: 25
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100.0%; Score 1287; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0;
                                                                                                                                                                                   Score 1287; DB 3;
Pred. No. 2.9e-125;
                                                                                                                                                                                 Query Match
100.0%; Score 1287; 1
Best Local Similarity 100.0%; Pred. No. 2.9
Matches 243; Conservative 0; Mismatches
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Patent No. 6284236
                                                                                                              MOLECULE TYPE: No. 6171787e
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  SEQUENCE CHARACTERISTICS LENGTH: 281 amino acid
                                                                     single
                                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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ORGANISM: human
                                                                                                                                        US-08-883-086-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180
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                                                                                                                                                                                                                                                       Length 281;
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Patent No. 6171787

GENERAL INFORMATION:
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 1100 Abbott Park Road
CITY: Abbott Park
STATE: 1100
                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                       100.0%; Score 1287; DB 3; 100.0%; Pred. No. 2.9e-125;
                                                                                                                                                                                                                                                                                                    0; Mismatches
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POTEMBORY, PISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
**LLEEAX: 415/925-5416
; TELERAX: 415/925-981
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acids TYPE: Amino Acid TYPE: Amino Acid TOPOLOGY: Linear US-08-780-496-1
                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 243; Conservative
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-883-086-10
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Query Match 100.
Best Local Similarity 100.
Matches 243; Conservative
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MOLECULE TYPE: protein
US-09-157-864-11
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GENERAL INFORMATION:
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                 SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 180
                                      159 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD 218
                                                                                         PILLIMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
                                                                                                                  61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
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GENERAL INCURCATION:
APPLICANT: YOUNG, PETER R.
APPLICANT: WASHALL, LISA A.
APPLICANT: RASHALL, LISA A.
APPLICANT: RASHALL, LISA A.
APPLICANT: RASHALL, LISA A.
APPLICANT: TRUNEH, ALENSEGED
ITILE OF INVENTION: TWOR NECROSIS FACTOR RELATED RECEPTOR,
ITILE OF INVENTION: TRANSECTOR
ITILE OF INVENTION: THAN NUMBER: 1999-06-15
PRIOR FILING DATE: 1997-06-12
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRACESO for Windows Version 3.0
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ORGANISM: HOMO SAPIENS
US-09-333-593A-6
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Best Local Similarity
Matches 243; Conserv
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US-09-157-864-11
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Application US/09157864

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Patent No. 6521228
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
ITILE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/09/157,864
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
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TELEX: 224401
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,1
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Gaps

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Indels

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99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
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                                                                              39 TNELKQMQDKYSKSGIACFLKEDDSYWDPNDESSMNSPCWQVKWQLRQLVRKMILRTSEE 98
                                                                                                                                          61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR
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100.0%; Pred. No. 2.9e-125;
tive 0; Mismatches 0;
         Mismatches
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US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739
; GENERAL INFORMATION:
; APPLICANT Rahkenazi, Avi J.
; APPLICANT Rahkenazi, Avi J.
; APPLICANT Relley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Schwall, Rabh H.
; TITLE OF INVENTION: Apo-2 Ligand
; TITLE OF INVENTION: Apo-2 Ligand
; TITLE OF LIGHT PELLING PRE-
; CURRENT PELLICATION NUMBER: US/09/582,450
; CURRENT PELLING DATE: 1998-01-15
; PRIOR FILING DATE: 1998-01-15
; PRIOR PILING DATE: 1998-01-15
; RUMBER OF SEQ ID NOS: 17
; SEQ ID NO :
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Matches 243; Conservative
         243; Conservative
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Sequence 118, Application US/09919039

Patent No. 6727066

GRNERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR PLING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 118

FENCEN.
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; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118
FILE REFERENCE: 2835-E

CURRENT APPLICATION NUMBER: US/09/825,563

CURRENT FILING DATE: 2001-04-02

RIOR APPLICATION NUMBER: 09/120,424

PRIOR FILING DATE: 1990-05-26

PRIOR FILING DATE: 1990-11-10

PRIOR FILING DATE: 1990-01-07

PRIOR FILING DATE: 1996-06-25

PRIOR APPLICATION NUMBER: 08/548,368

PRIOR APPLICATION NUMBER: 08/548,368

PRIOR PILING DATE: 1995-06-25

PRIOR PILING DATE: 1995-06-25

PRIOR PILING DATE: 1995-06-29

PRIOR PILING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 2
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Best Local Similarity 100.
Matches 243; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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; ORGANISM: human
US-09-825-563-2
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US-09-919-039-118
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                                                                  121 SGHSFLSNLHLRNGELVIHBKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Kathryn A. Anderson, Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
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APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANGERSON, KALHYN A.
REGISTRATION NUMBER: 32,172
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25-JUN-1996
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acid
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Matches 243; Conserv
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STATE: WA
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PCT-US96-10895-2
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100.0%; Pred. No. 2.9e-125;
ive 0; Mismatches 0;
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Batent No. 6828121

GENERAL INFORMATION:

APPLICANT: Chen, Christina Yu-Ching

TITLE OF INVENTION: BACTERIAL HOST STRAINS

FILE REFERENCE: P1804A11

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 60/256,162

PRIOR FILING DATE: 2000-12-14

PRIOR FILING DATE: 2000-12-14

PRIOR FILING DATE: 2000-12-14

FRIOR FILING DATE: 2000-12-14
                               Sequence 1, Application US/09934465
Patent No. 674668
GENERAL INFORMATION:
TITLE OF INVENTION: APO.2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT PILLING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR PILLING DATE: 1996-01-09
PRIOR FILING DATE: 1996-01-09
SEQ ID NO.1
SEQ ID NO.1
SEQ ID NO.1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
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Matches 243; Conservative
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Best Local Similarity
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US-10-011-125A-4
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99 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

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159 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRPQEEIKENTKNDKQMVQYIYKYTSYPD 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRPQEEIKENTKNDKQMVQYIYKYTSYPD 228
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JEDNICANT: SAVITZKY et al.,

TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS

FILE REFERENCE: 2786-0151P

CURRENT APPLICATION UMBER: US/09/569,611C

CURRENT FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 271

TYPE: PRT

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 22, 2005, 06:02:16
Job time : 28.8244 secs
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                                                                                                                                                                                                   RESULT 15
US-09-569-611C-30
Sequence 30, Application US/09569611C
Patent No. 6720182
GENERAL INFORMATION:
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Best Local Similarity 83.1
Matches 202; Conservative
                                                                                                                          LVG 243
                                                                                                                                                  LVG 281
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A,Residues: 1-30 <NOU2>

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ALIGNMENTS
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Pypothetical protein Vng0151c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: 102-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84175
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon Jung, K.H.; Alam, M.; Freitas, T.
FPTCC. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennisls, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lié, A;Reference number: A84160; MUD:20504483; PMID:11016950
A;Accession: F84175
A;Accession: F84175
A;Molecule type: DNA
A;Kesidues: 1-93 <STO>
A;Cross-references: UNIPROT:Q9HSN3; GB:AE004437; NID:g10579798; PIDN:AAG18770.1; GSPDB:GP:Construction of the construction of
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C;Date: 23-Nov-1991 #text_change 09-Jul-2004
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C;Date: 23-Nov-1991 #sequence 09-Jul-2004
C;Date: 23-Nov-1991 #sequence 09-Jul-2004
C;Date: 1991
C;Date: 23-Nov-1991 #sequence 09-Jul-2004
C;Date: 23-Nov-1991 #text_change 09-Jul-2004
C;Date: 23-Nov-1991

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                                                                                                                                                                                                                                                                                                                                     F;1-30/Domain: insulin chain B #status experimental <BCH>F;31-51/Domain: insulin chain A #status experimental <ACH>F;7-37,19-50,36-41/Disulfide bonds: #status predicted
A,Cross-references: UNIPROT:Q9TQY7
A,Accession: S6590
A,Molecule type: protein
A,Residues: 31-51 <NOU1>
C,Superfamily: insulin
C,Keywords hormone; pancreas
P,1-30,31-51/Product: insulin #status experimental <MAT>
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 8;
tive 0; Mismatches
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Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 EKGFYYI 184
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                                                                                                                                                                                 probable drug transport protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: 675599
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75599
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C;Genetics:
A;Gene: cg1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-643 <MHL>
A,Cross-references: UNIPROT: Q9RZ93; GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF1225
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Cell 91, 553-603, 1997
A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
A;Reference number: Z16556; MUID:98054002; PMID:9393853
A;Accession: T09076
A;Status: translated from GB/EMBL/DDBJ
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C;Species: Ornithorhynchus anatinus (duckbill platypus)
C;Species: Ornithorhynchus anatinus (duckbill platypus)
C;Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession. S63591; S63590
R;Nourse, A.; Treacy, G.B.; Shaw, D.C.; Jeffrey, P.D.
Biol. Chem. Hoppe-Seyler 377, 147-153, 1996
A;Title: Platypus insulin: indications from the amino acid sequence of significant diffe
A;Reference number: S63590; MUID:97021710; PMID:8868070
A;Accession: S63591
A;Molecule type: protein
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100.0%; Pred. No. 9.1;
:ive 0; Mismatches
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100.0%; Pred. No. 6.5;
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Best Local Similarity 100.
Matches 8; Conservative
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iCross references: UNIPROT:P09564; GB:M37271; NID:g180163; PIDN:AAA51953.1; PID:g180164; Aruffo, A.; Seed, B. MBO J. 6, 3313-3316, 1987
                                                                                                                                                                                                                                     A;Title: Molecular cioning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expr:
A;Reference number: S03520; MUID:88111517; PMID:3501369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: D9063
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguck A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Furocet, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001;
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Title: number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:099RD5; GB:BA000018; PID:g13702449; PIDN:BAB43590.1; GSPDB:GR
A,Experimental source: strain N315
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40807.
R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein sarH2 [imported] - Staphylococcus aureus (strain N315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat F;1-25/Domain: signal sequence #status preddicted <215.9. F:26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT>F;145-180/Region: 9-residue repeats (X-P-P-X-A-S-A-L-P)
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                                                                                                                                                                                                                                                                                                                                                                   CASS-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757; Genetics:
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      A; Reference number: A39016; MUID:91110576; PMID:1703303
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Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 32;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:119770; OMIM:186820
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A;Introns: 28/1
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Best Local Similarity 100.
Matches 7; Conservative
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A;Accession: T40807
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                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-240 <ARU>
                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-247 <KUR>
                                                                                                                                                                                                                                                                                                  A; Accession: S03520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nypothetical protein APE1675 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: 672548
S;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takahawa, B.; Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status; preliminary
                                                                                                                                                                                                                                                                                   C;Accession: C90304
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffkries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-107 <KUR>
A;Residues: 1-107 <KUR>
C;Coss-references: UNIPROT:Q97Y77; GB:AE006641; NID:g13814690; PIDN:AAK41690.1; GSPDB:G
C;Genetics:
A;Gene: SSO1462
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C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
R;Schanberg, L.E.; Fleenor, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991
A;Title: Isolation and characterization of the genomic human CD7 gene: structural simila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-155 <KAW>
A;Cross-references: UNIPROT:Q9YBC2; DDBJ:AP000062; NID:g5105244; PIDN:BAA80676.1; PID:d1
A;Expensimental source: strain K1
C;Genetics:
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                                                                                                                                                                                                    hypothetical protein SSO1462 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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100.0%; Pred. No. 15;
iive 0; Mismatches
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Matches 7; Conservative
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   POEEIKE 198
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                                                       FOEETKE
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192
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Query Match 2.5%; Score 7; DB 2.8est Local Similarity 100.0%; Pred. No. 41; Matches 7; Conservative 0; Mismatches
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0; Mismatches
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Best Local Similarity
Matches 7; Conserv
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Matches 7; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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H82736

H82736

H82736

Cypothetical protein XP0992 [imported] - Xylella fastidiosa (strain 9a5c)

Cypothetical protein XP0992 [imported] - Xylella fastidiosa

Cybate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

CyAccession: H82736

Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000

AyTitle: The genome sequence of the plant pathogen Xylella fastidiosa.

AyTete: for a complete list of authors see reference number A59328 below

AyAccession: H82736

AyAccession: H82736

AyAccession: Jaz - SIM>

AyAccession: Jaz - SIM>

AyAccession: H82736

AyAccession: H827
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Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Racincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors B. Ferreira, V.C.A.; Ferro, J.A.; Franco, M.C.; Franco, M.C.; Fronco, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laight, J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laight, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
                                     A Molecule type: DNA ** A Molecule type: DNA ** A Molecule type: DNA ** A Molecule type: Loss - A Molecule type: Loss - A Molecule treferences: UNIPROT: 094262; EMBL: AL032684; PIDN: CAA21798.1; GSPDB: GN00067; SPDB: A Molecule treference: Grain 972h-; clone pl p8B7 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical ser-thr rich protein - fission yeast (Schizosaccharomyces pombe) (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C'Species: Schizosaccharomyces pombe
C'Species: Schizosaccharomyces pombe
C'Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000
C'Accession: T38003
R'Ollver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z21760
A;Reference spraininary; translated from GB/EMBL/DDBJ
A;Residues: 1-Z63 < OLL>
A;References: EMBL: Z97209; PIDN: CAB10128.1; GSPDB: GN00066; SPDB: SPAC19G12.16c
A;Experimental source: strain 972h-; cosmid c19G12
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                                                                                                                                                                                                                                                                    A,Gene: SPDB:SPBP8B7.13
A,Map postition: 2
A,Introns: 54/1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBP8B7.13
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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2.5%; Score 7; DB 2. Best Local Similarity 100.0%; Pred. No. 33; Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 34;
tive 0; Mismatches
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A,Map position: 1
C,Superfamily: yeast glucan 1,4-alpha-glu
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Best Local Similarity 100.
Matches 7; Conservative
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A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, M.C.; D.A. B.A. R.G.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawssaki A; Authors: da Silva, A.C.R.; da Silva, F.R.; de Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; de Silva, A.M.; Silva Jr., W.A.; da Silvaire M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C; Accession: D71887
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Jres, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathor A;Reference number: A71800; MUD:99120557; PMID:9923682 A;Accession: D71887
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A;Status: Dreliminary
A;Molecule type: DNA
A;Residues: 1-329 <ARN>
A;Croselerences: UNIPROT:Q9ZKY9; GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD0636:
A;Experimental source: strain J99
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: G71465
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, A;Itle: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach A;Reference number: A71570; MUID:99000809; PMID:9784136
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A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
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;Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
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100.0%; Pred. No. 41;
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Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
Cipatcession: G90210
Cipatcession: G90210
Rishs, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-P.
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Median, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: G90210
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A,Residues: 1-404 «KUR»
A,Crossidues: UNIPROT:Q9UX27; GB:AE006641; NID:g13813800; PIDN:AAK40942.1; GSPDB:GP
C,Genetics:
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A,Molecule type: DNA
A,Residues: 1-420 <POB.
A,Cross-references: UNIPROT: P53616; EMBL:X86470; NID:g791101; PID:g791122
A,Cross-references: UNIPROT: P53616; EMBL:X86470; NID:g791101; PID:g791122
R,Bergez, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A,Fitle: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV fA,Reference number: S58711; MUID:96021608; PMID:8533472
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A,Residues: 1.420 cBER,
A,Kresidues: 1.420 cBER,
A,Cross-references: EMBL:U12141; NID:91314216; PIDN:AAA99645.1; PID:9994821
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A,Resrgez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A,Reference number: S62975
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C.Date: 08-Jul-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
C.Accession: S53916; SS8712; S62994; S62998; S63945
R.Pochlmann, R.; Philippsen, P.
aubmitted to the EMBL Data Library, April 1995
A.Reference number: S53896
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N;Alternate names: protein N2411; protein YNL066w; protein YNL1612
                                                                                                                                                                                                                                             hypothetical protein purF-2 [imported] - Sulfolobus solfataricus
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A,Status: nucleic acid sequence not shown; translation not shown
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Lbmitted to the Protein Sequence Database, April 1996
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100.0%; Pred. No. 50;
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Matches 7; Conservative
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A;Accession: S62998
                                                                157 DAEYGLY 163
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A; Residues: 1-420 < POW>
   234 DAEYGLY
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A; Cross-references: UNIPROT: O9PCZ3; GB:AE003988; GB:AE003849; NID:g9106653; PIDN:AAF8442
A; Cross-references: UNIPROT: O9PCZ3; GB:AE003988; GB:AE003849; NID:g9106653; PIDN:AAF8442
B; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Camrer, D.M.; Carrer, Fanelacto, GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr J.D.; Junqueira, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Matsukuma, A.Y.; Martins, E.A.; Matsukuma, A.Y.; Menck, C.F., Mirocca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; Ae Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Roda, A.C.; de Silve, R.C.; Falmieri, D.A.; Abuthors: da Silva, A.C.R.; da Silva, M.A.; Ga Sa, R.G.; Santelli, R.V.; Sawasak, A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; A.R.Eference number: A5928
                                                                                                                                                          RESULT 15
A81728
conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, M.Cleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUD:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A;Residues: 1-354 <TET>
A;Cross-references: UNIPROT:09PL80; GB:AE002289; GB:AE002160; NID:g7190254; PIDN:AAF3909
C;Genetics:
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C;Genetics:
A;Gene: XR1611
C;Superfamily: Escherichia coli hypothetical 48K protein (glnA-fdhE region)
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5. 49;
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100.0%; Pred. No. 44;
tive 0; Mismatches
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100.0%; Pred. No. 49;
ive 0; Mismatches
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Matches 7; Conserv
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A; Status: preliminary
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251
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Gaps

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A;Accession: G71272
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-427 <COL>
A;Cross-references: UNIPROT:083835; GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC65826
C;Genetics:
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Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H., Alam, M.; Freitas, T. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liference number: A84160; MuID:20504483; PMID:11016950
A;Accession: E84192
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I., C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
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A,Residues: 1-429 <ARN>
A,Cross-references: UNIPROT:Q9Z913; GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD1832
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A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
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C, Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase
F;237, Brinding site: pyridoxal phosphate (Lys) (covalent) #status predicted
F;374/Active site: Cys (cysteine persulfide intermediate) #status predicted
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A;Molecule type: DNA
A;Residues: 1-428 <STO>
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                                                                                     R;Poehlmann, R.; Philippsen, P.
Yeast 12, 391-402, 1996
A;Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12
A;Reference number: 563925; MUID:96267764; PMID:8701611
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-420 <POF>
A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PID:g791122
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
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     A; Cross-references: EMBL: Z71342; NID:g1301944; PID:g1301945; MIPS:YNL066w
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C;Keywords: mitochondrion
F;1-46/Domain: transit pendide (mitochondrion) #status predicted <TNP>
F;46-420/Product: SUN4 protein #status predicted <MAT>
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100.0%; Pred. No. 51;
iive 0; Mismatches 0; Indels
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A;Cross-references: SGD:S0005010; MIPS:YNL066w
A;Map position: 14L
                                                  A; Experimental source: strain S288C
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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Gaps

Query Match

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probable udp-n-acetylglucosamine pyrophosphorylase - fission yeast (Schizosaccharomyces r
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:094617; EMBL:AL035675; PIDN:CAB38688.1; GSPDB:GN00067; SPDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C27A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C;Accession: T19496
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47503, S17104; Sj3319
R;Knehr, M.; Thomas, H.; Arand, M.; Gebel, T.; Zeller, H.D.; Oesch, F.
                             Gaps
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A;Introns: 44/3; 87/2; 130/2; 164/3; 203/2; 273/3; 325/1; 369/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F07G11.3
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R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 475;
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-475 <WOO>
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A;Molecule type: DNA
A;Residues: 1-511 <WIL>
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. 57;
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  red. No. 54;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Harris, B. submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.5%; Score 7; DB 2
100.0%; Pred. No. 57;
iive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches
  100.08;
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epoxide hydrolase (EC 3.3.2.3),
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Best Local Similarity 100.
Matches 7; Conservative
  Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 TSEETIS 174
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                                                                                                                                 76 LLOSLCV 82
                                                                                     25 LLOSLCV 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: C27A7.2
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AF2539
manganese transport protein all7601 [imported] - Nostoc sp. (strain PCC 7120) plasmid pd C, Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Date: 14-Dec-3001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession: AF2539
C,Accession: AF2539
M: Tabata, M: Tabata, M: Tabata, M: Tabata, M: Tabata, M: Tabata,
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R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Ree. 28, 2311-2314, 2000
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A66491; MUID: 20330349; PMID: 10871362
A; Accession: C86512
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A;Experimental source: strain J138
C;Genetics:
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nak Res. 8, 205-213, 200
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; WUID:21595285; PMID:11759840
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A,Residues: 1-442 <KUR>
A,Cross-references: UNIPROT.Q8ZSB0; GB:AP003602; PIDN:BAB77244.1; PID:g17134686; GSPDB:G
A,Experimental source: strain PCC 7120
                 A;Accession: E81558
A;Molecule type: DNA
A;Residues: 1-429 cREA>
A;Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38415.1; PID:g718951
A;Experimental source: strain AR39, HL cells
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86512
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.;
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                                                                                                                                                              C;Genetics:
A;Gene: guaA; CP0599
C;Superfamily: GMP Bynthase (glutamine-hydrolyzing); trpG homology
F;11-194/Domain: trpG homology <TRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: guaA
C;Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology
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C;Superfamily: natural resistance-associated macrophage protein 1
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A; Reference number: A81500; MUID: 20150255; PMID: 10684935
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100.0%; Pred. No. 52;
iive 0; Mismatches
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100.0%; Pred. No. 52;
cive 0; Mismatches
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Matches 7; Conservative
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Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-429 <STO>
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A; Status: preliminary
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Query Match

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A;Residues: 1-710 <WIL>
A;Cross-references: UNIPROT:Q9XTSO; EMBL:Z99171; PIDN:CAB16314.1; GSPDB:GN00019; CESP:F47; A;Experimental source: clone F47G4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: AE3032
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:Q8U963; GB:AE008689; PIDN:AAL44675.1; PID:g17742302; GSPDB:G1A;Experimental source: strain C58 (Dupont)
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C; Species: Agrobacterium tumefaciens
C; Species: Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Accession: G9853
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Liu, E.; Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein Atu3866 [imported] - Agrobacterium tumefaciens (strain C58 C,Species: Agrobacterium tumefaciens
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
A;Introns: 20/1; 131/3; 220/2; 273/1; 380/2; 577/2
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100.0%; Pred. No. 91;
tive 0; Mismatches
                                                                                        submitted to the EMBL Data Library, September 1997
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A;Accession: T22360
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647 ILRTSEE 653
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hes 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-801 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: G98253
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-801 <KUR>
                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: CESP:F47G4.2
                             C, Accession: T22360
R; White, S.
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Matches
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A; Residues: 450-554 (ARA>
A; Cross-references: EMBL:X60328; NID:g55929; PIDN:CAA42898.1; PID:g55930
R; Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
FBRS Lett. 294, 19-22, 1991
A; Title: An impaired peroxisomal targeting sequence leading to an unusual bicompartmenta
A; Ritle: An impaired peroxisomal targeting sequence leading to an unusual bicompartmenta
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A,Residues: 1-565 <HEL>
A,Cross-references: UNIPROT:Q9KTU6; GB:AE004164; GB:AE003852; NID:g9655232; PIDN:AAF9395
A,Experimental source: serogroup O1; strain N16961; blotype El Tor
                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P80299; GB:X65083; NID:g402631; PIDN:CAA46211.1; PID:g402632
                                                                                                                                                                                                                                                                          A;Note: sequence extracted from NCBI backbone (NCBIN:136329, NCBIP:136330)
R;Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
submitted to the EMBL Data Library, September 1991
A;Description: The unusual bicompartimental distribution of cytosolic epoxide hydrolase
A;Reference number: $17104
A;Reference number: $17104
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Vibrio cholerae
(C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
(C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
(C;Accession, D: Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Status: preliminary
             A.Title: Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide A.Ritle Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide A.Reference number: A47503; MUID:93352557; PMID:8349641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: two-component sensor histidine kinase; sensor histidine kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sensor kinase citA VC0791 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; Score 7; DB 2;
100.0%; Pred. No. 66;
tive 0; Mismatches
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   Chem. 268, 17623-17627, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: S19319
A,Molccule type: mRNA
A,Residues: 448-554 <AR2>
C,Keywords: cytosol; ether hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100..
                                                                                                                                                             A; Molecule type: nucleic acid
A; Residues: 1-554 < KNE>
                                                                                                                                                                                                                                                          A; Experimental source: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477 KALGRKI 483
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                                                                                                                             A, Status: preliminary
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RESULT 29 T22360

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C;Genetics: A;Gene: AGR L 1958 A;Map position: linear chromosome

272 ASFFGAF 278

216 ASFFGAF 222

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A; Cross-references: UNIPROT: Q18284; EMBL: U40797; NID: g1065916; PID: g1065927; PIDN: AAB375 A; Experimental source: strain Bristol N2; clone C28C12 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 87, 249-255, 1990
A;Title: Characterization of the gene and an antigenic determinant of equine herpesvirus
A;Reference number: JH0109; MUID:90236317; PMID:1692002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: gp14
C;Superfamily: herpesvirus glycoprotein B
C;Superfamily: herpesvirus glycoprotein
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein 14 #status predicted <AGT>
F;87-979/Product: glycoprotein 14 #status predicted <AMT>
F;87-979/Region: hydrophobic
F;831-871/Region: hydrophobic
F;85,275,380,423,497,514,560,727,749,951,970/Binding site: carbohydrate (Asn) (covalent)
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: JH0109
A, Molecule type: DNA
A, Residues: 1-979 «GUO»
A, Cross-references: UNIPROT: P25218; GB: M34861; NID: G330900; PIDN: AAA46086.1; PID: G330901
A, Note: glycoprotein 14 is homologous to corresponding glycoprotein of pseudorabies, bov
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A;Introns: 18/3; 98/2; 173/2, 206/3; 298/3; 405/3; 488/3; 727/3; 761/1; 828/2
                                 hypothetical protein C28C12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: equine herpesvirus 1
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JH0109
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C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                             Rimiller, N. submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid C28C12. A; Reference number: 218387 A; Reference number: 218387
                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-926 <MIL>
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R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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|22 DEESMNS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: C28C12.10
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D90183
Thro-dependent helicase [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90183
R;She, Q; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; ChanJong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90183
A.Cross-references: UNIPROT:08U963; GB:AE007870; PIDN:AAK89553.1; PID:g15159435; GSPDB:G
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C;Genetics:
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A,Introns: 49/3; 144/1; 319/2; 376/3; 484/2; 540/3; 573/2; 612/3; 720/3; 776/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apporthetical protein E03A3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20430
R;Gardner, A
Bubmitted to the EMBL Data Library, October 1994
A;Reference number: Z19Z74
A;Reference number: Z19Z74
A;Reference prelimitary; translated from GB/EMBL/DDBJ
A;Residues: L909 <WIL>
A;Residues: 1-809 <WIL>
                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0
                                                                                                                                                      Query Match 2.5%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.5%; Score 7; DB 2;
Local Similarity 100.0%; Pred. No. 92;
les 7; Conservative 0; Mismatches
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A; Experimental source: clone E03A3

C;Genetics: A;Gene: CESP:E03A3.2

756 EYGLYSI 762

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236 EYGLYSI 242

Query Match Best Local S: Matches 7

Conservative

Local Similarity 1es 7; Conserva

A; Gene: SS00394

Query Match

A Status: preliminary A Molecule type: DNA A;Residues: 1-913 <KUR>

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RESULT 34

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: UNDA
A;Foresidues: 1-1414 *CGRE>
A;Cross-references: UNDRROT:O76411; EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN00023; CESP:7
A;Experimental source: strain Bristol N2; clone T10H9
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A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A.Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A.Reference number: A64300; MuID:96337999; PMID:8688087
                                                                                                                                                                                                                                  A;Map position: 1
A;Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3; 826
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
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A;Introns: 56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3; 520/2; 569
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A;Cross-references: EMBL:281516; PIDN:CAB04207.1; GSPDB:GN00019; CESP:F26H9.8 A;Experimental source: clone F26H9
C;Genetics: A;Gene: CESP:F26H9.8
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C,Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C,Accession: E64477
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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A;Gene: CESP:T10H9.2
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Best Local &
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T19214
DD-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - Caenorhabd C; Species: Caenorhabdtis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T19214; T21444
R; Barlow, K.
submitted to the EMBL Data Library, November 1996
A; Reference number: Z19091
A; Accession: T19214
A; Accession: T19214
A; Accession: T19214
A; Realuminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1377 < WIL>
A; Residues: 1-1377 < WIL>
A; CESP: F2
A; 
     A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: E88465
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-982 <STO>
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A,Residues: 1-1014 <SEE>
A,Cross-references: UNIPROT:Q9Z507; EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCOED
A,Experimental source: strain A3(2)
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.Genetics:
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A;Reference number: 221581
A;Stecession: TJS601
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: T21444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1377 <WI2>
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Matches 7; Conservative
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A;Map position: 3
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A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A/Itle: Complete genome sequence of Naisseria meningitidis serogroup B strain MC58.
A/Accession: G81044
A/Status: preliminary
A/Aolecule type: DA
A/Status: preliminary
A/Aolecule type: DA
A/Accession: G8104
A/Acce
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C; Accession: B81989
R; Parkhili, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MuID:20222556; PMID:10761919
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A;Molecule type: DNA
A;Residues: 1-2015 <PAR>
A;Cross-references: UNIRROT:09JRD2; GB:AL162753; GB:AL157959; NID:97379120; PIDN:CAB8397<br/>A;Experimental source: serogroup A, strain 22491
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N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS1
a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: Murray Valley encephalitis virus
C;Date: 30-Jun-1988 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A24635; A60288
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A,Reference number: A60288, MUID:91102934, PMID:1702914
A,Accession: A60288
A,Molecule type: genomic RNA
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A;Residues: 1-1780 cDAL>
A;Crose-references: UNIPROT:P05769; GB:X03467; NID:g59329; PIDN:CAA27184.1; PID:g755731
R;Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.M.; Dalgarno, L.
Virus Genes 4, 197-213, 1990
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J. Mol. Biol. 187, 309-323, 1986
A;Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome:
A;Reference number: A24635; MUID:86200215; PMID:3009829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.5%; Score 7; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0
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Best Local Similarity 100.
Matches 7; Conservative
    287, 1809-1815, 2000
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A;Gene: NMA0688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                calcium channel alpha-1 chain, L-type - Stylophora pistillata
Calcium channel alpha-1 chain, L-type - Stylophora pistillata
C;Species: Stylophora pistillata
C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43262
R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J
Gene 227, 157-167, 1999
A;Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylc
A;Accession: T43262
A;Accession: T43262
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1891 <ZOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 42
B81192
Chamagglutinin/hemolysin-related protein NMB0497 [imported] - Neisseria meningitidis (str
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81192
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Carndi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
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A;Residues: 1-1975 <TET>
A;Cross-references: UNIPROT:Q9K0S7; GB:AE002406; GB:AE002098; NID:g7225720; PIDN:AAF4092
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:097017; EMBL:U64465; NID:g4204977; PID:g4204978; PIDN:AAD114
Genetics:
A;Genetics: ACHL
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
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G81044
hemeolysin-related protein NMB1779 [imported] - Neisseria meningitidis (str.)
hemeoglutinin/hemolysin-related protein NMB1779 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G8104
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.F.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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FLKEDDS 1627
IFELKEN 253
                                                        ||||||||||
|FELKEN 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 FLKEDDS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
247
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C;Genetics:
A;Gene: atp8
A;Generic code: SGC2
C;Superfamily: yeast H+-transporting ATP synthase protein 8
C;Superfamily: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Althoretical protein as12397 [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120
A,Note: Nostoc sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
R.Staneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: UNIPROT: QBYUF3; GB: BA000019; PIDN: BAB74096.1; PID:g17131489; GSPDB:GPA; Experimental source: strain PCC 7120
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R;Handrikman, A.J.; van Leeuwen, C.; Kok, J.; Vos, P.; de Vos, W.M.; Venema, Appl. Environ. Microbiol. 56, 1890-1896, 1990
A;Title: Insertion elements on lactococcal proteinase plasmids.
A;Reference number: A60157; MUID:90343335; PMID:2166472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 2 (prtM 5' region) - Lactococcus lactis subsp. cremoris C;Species: Lactococcus lactis subsp. cremoris C;Date: 03-Mar-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Score 6; DB 2; Length 56; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                             2.1%; Score 6; DB 2
100.0%; Pred. No. 88;
tive 0; Mismatches
A; Experimental source: strain ad7-50h
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Best Local Similarity 100.
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-56 < HAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 IFTVLL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 FLSNLH 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 IFTVLL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: as12397
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S78202
H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - fission yeast (Schizosacchar C:Species: mitochondrion Schizosaccharomyces pombe
C;Becession: S78202
C;Accession: S78202
C;Accession: S78202
R:Lang, B.F.
submitted to the EMBL Data Library, August 1990
A;Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe: chizosaccharomyces pombe and Aspergillus nidulans.
A;Reference number: S78195
A;Accession: S78202
A;Accession: S78202
A;Recession: S78202
A;R
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A;Cross-references: UNIPROT:024522; EMBL:U95216; NID:g2443456; PIDN:AAB71382.1; PID:g244
C;Genetics:
A;Gene: EREBP1
                            C; Superfamily: yellow fever virus genome polyprotein
C; Superfamily: yellow fever virus genome polyprotein; glycoprotein; nonstructural protein;
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein precursor #status predicted <GLC>
F;126-292/Product: membrane protein precursor #status predicted <GLC>
F;126-217/Domain: nonterminal signal sequence #status predicted <GLC>
F;18-292/Product: membrane protein #status predicted <GLN>
F;293-792/Product: envelope protein #status predicted <TN>
F;293-793/Product: envelope protein #status predicted <NS>
F;391-205/Product: nonstructural protein NS1 #status predicted <NS2>
F;1206-1372/Product: nonstructural protein NS2 #status predicted <NS2>
F;1504-2122/Product: nonstructural protein NS2 #status predicted <NS3>
F;1697-1104/Region: nucleotide-binding motif A (P-loop)
F;1784-1789/Region: DEAH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ethylene responsive element binding protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04365
R;Kim, C:Y:; Jeong, S:Y:, Choe, M.S.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
submitted to the EMBL Data Library, March 1997
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F;2415-2529/Product: nonstructural protein NS4b #status predicted <N8B>
F;2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>
F;73,140,446/Binding site: carbohydrate (Asn) (covalent) #status predicted
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ches 0; Indels
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A;Accession: T04365
A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 3.3
tive 0; Mismatches
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100.0%; Pred. No. 86;
:ive 0; Mismatches
    A;Residues: 1504-1778,'V';1780-3434 <LEE>
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Best Local Similarity 100..
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Matches 6; Conservative
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A;Cross-references: SGD:S0007235
A;Map position: 4R
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Best Local Similarity 100.4
Matches 6, Conservative
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A,Residues: 1-85 <HAY>
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A; Residues: 1-89 < DUZ>
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A; Status: preliminary
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A;Gross-references: UNIPROT:Q8U558; GB:AE007869; PIDN:AAK87924.1; PID:g15157324; GSPDB:G
C;Genetics:
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A; Molecule type: DNA
A; Residues: 1-64 «KUR>
A; Cross-references: UNIPROT: Q8ZJB1; GB: AL590842; PIDN: CAC89066.1; PID: g15978306; GSPDB: G
A; Genetics:
A; Genetics:
C; Superfamily. when
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CiSpecies: Yersinia pestis

CiDate: O2-Nov-2001 #sequence_revision O2-Nov-2001 #text_change O9-Jul-2004

CiAccession: AG0025

R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-577, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Status; preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 62;
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2.1%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0;
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A,Map position: circular chromosome
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A;Molecule type: DNA
A;Residues: 1-62 <KUR>
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hypothetical protein EC84963 [imported] - Escherichia coli (strain O157:H7, substrain RI: C;Species: Escherichia coli (c;Date: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 09-Jul-2004 [C;Accession: C]21249 [S;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Hattle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <PAR>A;Cress-references: GB:AL513382; PIDN:CAD02513.1; PID:g16503375; GSPDB:GN00176
C;Genetics:
A;Gene: STY2363
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C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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2.1%; Score 6; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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2.1%; Score 6; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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R;Du, Z.
submitred to the EMBL Data Library, June 1995
A;Description: The sequence of S. cerevisiae cosmid 9476.
A;Reference number: S61148
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Fitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                       A;Accession: G91248
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 AHAY>
A;Especimental source: uniprof; GB:BA000007; PIDN:BAB38382.1; PID:g13364435; GSPDB:GP
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable cytochrome C fragment [imported] - Sinorhizobium meliloti (strain 1021) magaplas C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2011 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: C95337
R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot; A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Robecule type: DNA
A;Resdues: 1-102 <KUR>
A;Rosiques: 1-102 <KUR>
A;Cross-references: UNIPROT: 092289; GB:AE006469; PIDN:AAK65261.1; PID:g14523712; GSPDB:GR
A;Experimental source: strain 1021, megaplasmid p5ymA
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293; 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, W.L.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Contents: annotation
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N;Alternate names: hypothetical protein Y (pbpF 5' region)
C;Species: Bacillus subtilis
C;Date: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change O9-Jul-2004
C;Accession: E69832; C40614
R;Kunst, F: Ogaamwara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertert
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 6; Conservative
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C; Accession: G91248
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                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: EC84959
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C; Species: Agrobacterium tumefaciens
C; Date: 11.-Jan.-2002 #sequence_revision 11.-Jan.-2002 #text_change 09-Jul-2004
C; Accession. AE3202
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell S; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Cross-references: UNIPROT:Q8UJV4; GB:AE008687; PIDN:AAL46059.1; PID:g17743819; GSPDB:G
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9KUJ3; GB:AE004139; GB:AE003852; NID:g9654953; PIDN:AAF9369
A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                   conserved hypothetical protein VCO527 [imported] - Vibrio cholerae (strain N16961 serogra C.species: Vibrio cholerae C.bate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C.Accession: B82311
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                                                                                                                                                                                                                                                                             Ribeidelberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalamos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Title: Ag2035; MUID:20406833; PMID:10952301
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A,Accession: AE3205
A,Status: preliminary
A,Molecule type: DNA
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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100.0%; Pred. No. 1...
0; Mismatches
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100.0%; Pred. No. 1.6
:ive 0; Mismatches
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A,Map position: 1
C,Superfamily: hypothetical protein HI0673
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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A; Residues: 1-96 <HEI>
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A;Gene: tnp
A;Genome: plasmid
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R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Bur. J. Immunol. 20, 771-777, 1990

A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies A;Reference number: 809955; MUID:90269328; PMID:2347362

A;Recession: 809964

A;Rocession: 8099664

A;Molecule type: mRNA
A;Residues: 1-107 < REI>
A;Cross-references: EMBL:XS1852; NID:955393; PIDN:CAA36145.1; PID:9930229
C;Reywords: heterotetramer; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibcose transporter isoform 1, GLUT 1 - mouse (fragment)
Cispecies: Mus musculus (house mouse)
Cispecies: The musculus (house mouse)
Cispecies: The bollogy # #sequence_revision 17-Feb-1994 #text_change 24-Sep-1999
Ciscossion: A44887
Rifogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Thomography and the transporter gene expression in early mouse embryos.
A; Reference number: A44887; MUD:92111400; PMID:1755007
A; Reference number: A44887; MUD:92111400; PMID:1755007
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: Tilo7 - AHOG
A; Ross-references: GB:577924; NID:9242127; PIDN:AAB20846.1; PID:9242128
A; Resperimental source: embryo
A; Note: this sequence is inconsistent with the nucleotide translation
C; Superfamily: glucose transport protein
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and capace number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84012
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Match 2.1%; Score 6; DB 2; Length 107; Local Similarity 100.0%; Pred. No. 1.8e+02; es 6; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
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A, Cross-references: UNIPROT: 09K8V0,
A, Experimental source: strain C-125
C, Genetics:
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Matches 6; Conservative
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Matches 6; Conserv
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                              A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, F.; Koningstein, G.; Krogh, S.; Kumita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadade, Y.; Sato, T.; Saronlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffens, F.; Skiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wight, A.; Yamanoto, H.; Yamanoto, K.; Yata, K.; Yoshida, K.; Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Areference number: A69580; MUD:98044033; PMID:9384377
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Rosesidues: 1-104 «KUN»
A; Rosesidues: 1-104 «KUN»
A; Rosesidues: UNIPROT:P38048; GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12849.
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B86818
hypothetical protein ypiJ [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: R6818
R;Bolotin, A.; WinoKer, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Accession: B86818
A;Accession: B86818
A;Accession: B86818
A;Accession: B6818
A;Accession: Bactiminary
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V. Bacteriol. 175, 4870-4876, 1993
A;Title: Cloning, mucleotide sequence, and regulation of the Bacillus subtilis pbpF gene
A;Reference number: A40614; MUID:93328693; PMID:8335642
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Ig kappa chain V-J region (105-2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09964
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100.0%; Pred. No. 1.7e+02;
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o, Mismatches
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Matches 6; Conservative 0; Mismatches
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C;Genetics:
A;Gene: yhgB
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Nature 390, 249-256, 1997
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A; Residues: 1-67 < POP>
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1.116 < STO>
A;Cross-treferences: UNIPROT:Q51450; GB:AE004801; GB:AE004091; NID:g9950011; PIDN:AAG0722:
A;Experimental source: strain PAO1
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-17 <KUR>
A,Residues: 1-17 <KUR>
A,Cross-references: UNIPROT:Q97GY7; GB:AE001437; PIDN:AAK80185.1; PID:g15025227; GSPDB:GP
R;Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A;Title: Structural differences in a single gene encoding the V-kappa-Ser group of light
A;Reference number: A94141; MUID:87067464; PMID:3097643
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probable chaperone PA3842 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A, Molecule type: DNA
A, Residues: 1-115, E00y-
A, Residues: 1-115, E00y-
A, Experimental source: strain BALB/c
G, Genetics:
A, Introns: 17/1
C, Superfamily: immunoglobulin V region; immunoglobulin homology
E, 1-20/Domain: signal sequence #status predicted <SIG-
F, 21-115/Product: Ig kappa chain V region Ser-b #status predicted <MAT>
F, 36-110/Domain: immunoglobulin homology 
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C;Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein
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2.1%; Score 6; DB 2; Lei
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0;
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21 PNDEES 26
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A.Reference number: AB2577; MUID:21608550; PMID:11743193
A.Accession: AC2887
A.Accession: AC2887
A.Accession: AC2887
A.Residues: preliminary
A.Residues: 1-112 < KUR>
A.Residues: 1-113 < KUR>
A.Residues: 1-113 < KUR>
A.Residues: 1-114 < KUR>
A.Residues: 1-144 < KUR>
A.Residues: 1-144 < KUR>
A.Residues: 1-144 < KUR>
A.Residues: 1-144 < KU
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: H97662
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
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A,Molecule type: DNA
A,Residues: 1-112 <KCR>
A,Cross-references: UNIPROT:Q8UCG1; GB:AE007869; PIDN:AAK88257.1; PID:g15157717; GSPDB:G
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                conserved hypothetical protein Atu2526 [imported] - Agrobacterium tumefaciens (strain C,Species: Agrobacterium tumefaciens C,Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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100.0%; Pred. No. 1.8
tive 0; Mismatches
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A;Map position: circular chromosome
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Matches 6; Conservative
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                170 RNGELV 175
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                                                                                     38 RNGELV 43
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C;Accession: AH0043

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E Nature 413, 523-527, 2001

A;Reference anguence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Residues: preliminary

A;Residues: 1-128 «KUR»

A;Residues: 1-128 «KUR»

A;Cross-references: UNIPROT:QBZIX2; GB:AL590842; PIDN:CAC89211.1; PID:g15978450; GSPDB:GP
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ribose ABC transporter permease protein rbsD [imported] - Lactococcus lactis subsp. lactis f58e29

ribose ABC transporter permease protein rbsD [imported] - Lactococcus lactis subsp. lactis (5.5pecies: Lactococcus lactis subsp. lactis
C;5pecies: Lactococcus lactis subsp. lactis
C;5pecies: Lactococcus lactis subsp. lactis
C;5pecies: 13. marcker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis acid ba
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2.1%; Score 6; DB 2; Length 128;
Local Similarity 100.0%; Pred. No. 2.1e+02;
les 6; Conservative 0; Mismatches 0; Indels
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C;Superfamily: Bscherichia coli hypothetical protein o128
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C,Superfamily: fucose operon U protein
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Matches
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D64559
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C; Species: Orgyja pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C; Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C; Accession: J02032
R;Russell, R.L.Q.; Rohrmann, G.F.
J. Gen. Virol. 74, 1191-1195, 1993
A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyja pseudotsug A;Reference number: PQ0633; MUID:93286576; PMID:8389803
A;Accession: J02032
A;Accession: J02032
A;Accession: J02032
A;Resiques: 1-119 <RUS>
A;Resiques: 1-119 <RUS>
A;Coss-references: UNIPROT:Q05122; DDBJ:D13375; NID:g222217; PIDN:BAA02641.1; PID:g2222
C;Superfamily: Orgyla pseudotsugata multicapsid nuclear polyhedrosis virus lambda 208 pr
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R;Accession: B9803
C;Shiba, T; Hattori, M; Kobayashi, N.; Sawano, T.; Tunoue, R.; Kaito, C.; Sekimizu, K.;
C;Shiba, T; Hattori, M; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Residues: 1-122 <KURA
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A,Experimental source: strain N315
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D89803
Conserved hypothetical protein SA0358 [imported] - Staphylococcus aureus (strain N315)
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probable lipoprotein YPO0352 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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                                                                                                                                              2.1%; Score 6; DB 2; Length 117;
100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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A; Experimental source: Clostridium acetobutylicum ATCC824 C; Genetics: A;Gene: CAC2228
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0
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Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                             171 NGELVI 176
                                                                                                                                                                                                                                                                                                                                                      91 NGELVI 96
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A,Gene: SA0358
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probable regulatory protein STY3045 [imported] - Salmonella enterica subsp. enterica ser C; Species: Salmonella enterica subsp. enterica serovar Typhi C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Dacession: Ac0855 R; Accession: Ac0855 R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Cunnerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Skelton, J.; Stevens, K.; A; Hitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; WUID:21534947; PMID:11677608 A; Accession: Ac0855 A; Actatus: preliminary A; Molecule type: DNA A; Resistant Salmonella enterica serov A; Resistant Salmonella enterica seros A; Constant Salmonella enterica seros A; Constant Salmonella enterica Salmonella enterica enterica seros C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Rv3069 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-UNL-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: F70650
R;Oble, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUD:98295987; PMID:9634230
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A, Residues: 1-132 <COL>
A, Cross-references: UNIPROT: P95089; GB: Z83866; GB: AL123456; NID: G3261691; PIDN: CAB06254. A, Experimental source: strain H37Rv C; Genetical source: A, Golderine Ray Strain H37Rv C; Genetical source: C; Golderical Strain H37Rv C; Golderical Strain H37Rv C; Golderical Strain H37Rv C; Golderical Strain H37Rv C; Golderical Strain M31523
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2.1%; Score 6; DB 2; Length 132;
100.0%; Pred. No. 2.1e+02;
:ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 6; Conservative
Query Match
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                                                                                                                                                      194 EEIKEN 199
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Q83tul staphylococ Q6gbc3 staphylococ Q6git5 staphylococ Q9n8d4 trypanosoma	Q7r3y3 giardia lam Q8p7k6 xanthomonas		acidovora bradyrhiz vibrio vu		Q688b3 acidovorax P09564 homo sapien		Q731u3 scapnylococ Q7a004 staphylococ	Q6g6h6 staphylococ 094262 schizosacch	rhizobium bacillus	Qelfe4 bacillus th Qehfe4 bacillus th Qerolo mus musculu		QQQXW4 BLEEDCOCC QBe313 Streptococc Q6k2p1 picrophilus Q6z6a7 oryza sativ	09vi33 drosophila	Q9pen6 xylella ras Q9zky9 helicobacte	084846 chlamydia t	Q9p180 chlamydia m Q9ave6 oryza sativ	P90756 caenorhabdi	Q8wpj2 mytilus edu Q6glf3 xenopus tro				Q7n5q0 photorhabdu	Q91thl arabidopsis O68ss3 pleurotus d	pleuroti	xylel xylel	Q9h766 homo sapien Q9ux27 sulfolobus			Q8k5j7 streptococc Q8e179 oryza sativ	Q8kir0 pseudomonas Q8kiu0 pseudomonas		
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compuge	protein search, using sw model	June 22, 2005, 06:07:26 ; Search t: (without 822.253	US-10-662-429-2 281 1 MAMMEVQGGPSLGQTCVLIVNEH	OLIGO Gapop.60.0 , Gapext 60.0	1612378 seqs, 512079187 residues		hits satisfying chosen parameters:	ength: 0 ength: 2000000000	Listing first 100 summaries	UniProt_03:* 1: uniprot sprot:*	<pre>2: uniprot_trembl:*</pre>	io. is the number of results predicted by reater than or equal to the score of the derived by analysis of the total score di	SUMMARIES	Query	acch bength bb 1D	100.0 281 1 TN10 HUMAN 18.5 63 2 Q6JSD9	5.0 291 1	4.6 304 2 3.6 299 2	2.8 155 2.8 465	2.8 473 2	2.8 475 2	2.8 643 2 2.8 939 2	2.8 950 2 2.8 1248 2	2.5 39 2	2.5 73 2 Q7UR	2.5	2.5	2.5 96 1	2.5 106 2.5 107	2.5 112 2 2.5 121 2	2.5 123 2	2.5 134 2 2.5 155 2
	OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Word size :	Total number of	Minimum DB seg l	Post-processing:	Database :		Pred. No. is t score greater and is derived			. score	281 52														26 7		

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garzen B.D., Mullahy S.J.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Whiting M., Madan A., Young A.C., Bloychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96111955; PubWed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.; Identification and characterization of a new member of the TNF family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;
Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
Kelley R.P., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";
Mol. Cell 4:563-571(1999).
                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
52-0CT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
Name=TNFSF10; Synonyms=APO2L, TRAIL;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                          "Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."; J. Biol. Chem. 271:12687-12690(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10542098; DOI=10.1038/14935; Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Screaton G.R.; "Structure of the TRAIL-DRS complex reveals mechanisms conferring specificity in apoptotic initiation."; Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96278649; PubMed-8663110; DOI=10.1074/jbc.271.22.12687;
Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
AFDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                         281 AA.
                                                                                                                                                                                                                                                                                                                 that induces apoptosis.";
Immunity 3:673-682(1995).
                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi A.;
                                         HUMAN
                                                     P50591;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM, 603589; -
GO; 0005887; C:integral to plasma membrane; TAS.
GO; GO:0005887; C:soluble fraction; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:receptor binding; TAS.
GO; GO:00073123; P:positive regulation of 1-kappaB kinase/NF-k. . .; IEP.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006983; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR003886; TNF_like.
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
Sung Y.C., Oh B.-H.;
"2.8 A resolution crystal structure of human TRAIL, a cytokine with
selective antitumor activity.";
Immunity 11:25-261(1999).
I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10B/TRAILR4 and
possibly also to TNFRSF11B/OFG. Induces apoptosis. Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-i- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
                                                                                                                                                                                                                                                                                                                                                                                induce apoptosis. COPACTOR: Binds 1 zinc ion and one anionic solvent molecule per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure; Apoptosīs; Cytokine; Metal-binding; Signal-anchor;
Transmembrane; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane
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Signal-anchor for type II
protein (Potential).
Extracellular (Potential).
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PDB; 1DGG; X-ray; A/B/D=114-281.
PDB; 1D2Q; X-ray; A=114-281.
PDB; 1D4V; X-ray; B=119-281.
PDB; 1DGG; X-ray; A=91-281.
PDB; 1DGG; X-ray; A=91-281.
PDB; 1DGS; X-ray; A=91-281.
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Probom, P0002012; TNF subf; 1
SMART, SMO0207; TNF, 1.
PROSITE; PS000251; TNF 1; 1.
PROSITE; PSS0049; TNF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homotrimer.
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Immunity 3:673-682(1995).
-!- FUNCTION: -Cytokine that binds to TNFRSF10A/TRAILR1,
-INFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
may be modulated by binding to the decoy receptors
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goodwin R.G.;
"Identification and characterization of a new member of the TNF family
                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=96111955; Pubmed=8777713; DOI=10.1016/1074-7613(95)90057-8; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Tumor necrot is fact in a sequental annotation update of the control is a sequental annotation (TNF-related apoptosis inducing ligand) (TRAIL protein)
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-i- TISSUB SPECIFICITY: Widespread.
-i- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:001620; C:membrane; IEA.
GO; GO:00164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; F:tumor necrosis factor receptor binding; IEA.
InterPro; IPR006951; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_subf.
ProDom; PD002012; TNF subf.
ProDom; PD002012; TNF subf; 1.
PROSITE; PS00251; TNF 1; UNKNOWN_1.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                          STRAIN-DA;
Mueller A.M., Giegerich G.;
Mueller A.M., Giegerich G.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AXIIS:78; AAM49797.1;
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32979 MW, CA4F5B5D7C833FEC CRC64;
           01-MAR-2004 (TrEMBLrel. 22, Last sequence update) TNF-related apoptosis inducing ligand. Sattus norvegicus (Rat). Bukarvers water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 29; DB 2; Le
100.0%; Pred. No. 1.3e-21;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Tnfsf10; Synonyms=Trail;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TN10 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TN10_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
     SO DE RESERVA DE LA PERSONA DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYYIYSQTYFRFQEEIKENTKODKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLIMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                          1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung carcinoma;
Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNELKOMODKYSKSGIACFLKEDDSYMDPNDEESMNSPCWOVKWOLKOLVRK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWOLROLVRK 90
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine tumor necrosis factor ligand superfamily member 10
                                                                                                                                                                                                                                                                          100.0%; Score 281; DB 1; Length 281; 100.0%; Pred. No. 1e-287; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 52; DB 2; Length 63; 100.0%; Pred. No. 1.7e-46; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kere J.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                          DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                          32509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY312579; AAR16184.1;
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.5%;
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                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
234
255
255
265
265
265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                       281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
233
237
252
255
263
266
270
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                                                                                                                                                                                       STRAND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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Q8K3G0,
TURN
                                                   TURN
                                                                                                          HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60SL90
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Matches
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RESULT 3
Q8K3G0
ID Q8K3G

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Gaps

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Length 287;

Gaps ö

Indela

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Mismatches

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Matches 13; Conservative
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                                                                                  RESULT 6
                                                                                               Q6DHG9
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the European Bioinformatics Institute. There are no restrictions on its way wise by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
Sayed A.A., Horluchi H., Furusawa S., Matsuda H.;
"Molecular Cloning and Characterization of Chicken Tumor Necrosis
Pactor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing Ligand (TRALL).";

Inducing Ligand (TRALL).";

Inducing Ligand (TRALL).";

Inducing Ligand (TRALL).";

Rembi, Abali4679; BAC79267.1; -...

HSSP; P5059; 1D20.

GO; GO:0006164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006955; P:immune response; IEA.

R InterPro; IPR006052; TWF family.

R InterPro; IPR008983; TWF like.

R InterPro; IPR008983; TWF like.

R Probom; PF00229; TWF; Bubf; 1.

R PROSITE; PS00221; TWF: 1.

R PROSITE; PS00251; TWF: 2; 1.

R PROSITE; PS00251; TWF: 2; 1.

C SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;
                                                                                                                                                                                                                         Signal anchor for type II membrane protein (Potential).

Extracellular (Potential).

N-linked (GlcNAc. . .) (Potential).

3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6%; Score 13; DB 2; Length 304; 100.0%; Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                               5.0%; Score 14; DB 1; Length 291;
100.0%; Pred. No. 8.9e-06;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor related apoptosis inducing ligand.
                                                                                                                                                                                                                  Cytoplasmic (Potential).
                                                                                                                                                                            PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Appptosis; Cytokine; Signal-anchor; Transmembrane.
DOMALN
18 Signal-anchor for typ
                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                           MGD; MGI:107414; Thfsf10.
InterPro; IPR006052; TNF_family.
InterPro; IPR00393; TNF_like.
InterPro; IPR00333; TNF_subf.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf; 1.
SMART; SM02207; TNF; 1.
                                                                                                                                                                                                                                                               52 52 N
291 AA; 33477 MW;
                                                                      EMBL; U37522; AAC52345.1; -.
HSSP; P50591; 1D2Q.
                                                                                                                                                                                                                                                                                                                                                             217 VQYIYKYTSYPDPI 230
                                                                                                                                                                                                                                                                                                                                                207 VQYIYKYTSYPDPI 220
                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                    33
                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus.
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 07T1F2
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
Q7T1F2
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Best Local Similarity

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Attaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A ploking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan R.J., Malan S., Gunzarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rakeabey R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio (Zebrafish) (Danio rerio).
Brachydanio Buteleostomi;
Brachydanio Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC076005; AAH76005.1; -...
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005955; P:immune response; IEA.
InterPro; IPR006055; TNF family.
InterPro; IPR00893; TNF family.
InterPro; IPR00893; TNF like.
Pfam; PF00229; TNF; II.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 10; DB 2; Length 299;
100.0%; Pred. No. 0.15;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33526 MW; BA776793D2F11ED5 CRC64;
                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                  299 AA.
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00251; TNF 1; 1. PROSITE; PS50049; TNF 2; 1. SEQUENCE 299 AA; 33526 MM
180 GEYYIYSQTYFRF 192
                                                                  184 GFYYIYSOTYFRF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednences.
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Les 10, Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 YXIXSQTYFR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 YYIYSOTYFR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Zgc:92320.
Name=zgc:92320;
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complexity of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        high pressure adaptations.",
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378669; CAG20488.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid-polyamine transporter activity; GO; GO:0006866; P:amino acid transport; IEA.
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Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.
                                                                                                                                                                                                                                                                                                                                                            STRIN-YS-314;
MEDLINE-2273752; PubMed=12840036; DOI=10.1101/gr.1285603;
Mishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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Name=ECS3960; OrderedLocusNames=PBPRA2086;
Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
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EMBL, AP005214; BACL6908.1; -.
Complete proteome; Hypotherical protein.
SEQUENCE 473 AA; 52745 MW; 9BBP8DBDAA8E249 CRC64;
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PROSITE; PS00589; PTS HPR SER; UNKNOWN 1.
Complete protecome; Transmembrane; Transport.
SEQUENCE 474 AA; 51903 MW; FAIDIAEBEEBFCF95 CRC64;
                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
OrderedLocusNames=CE0098;
Corynebacterium efficiens.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 30;
tive 0; Mismatches
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100.0%; Pred. No. 30;
tive 0; Mismatches
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Interpro; IPR002114; HPr_SerP_S.
Interpro; IPR004841; Permease_region.
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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10 Q6/LQB8
AC Q6/LQB1
DT 05-JUJ
DT 05-
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Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
'Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).

EMBL; AP006841; BAD48864.1; -.
SEQUENCE 155 AA; 17962 MW; B66A33ABAP0DDB63 CRC64;
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MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
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                                                                                                                                                                                                                                             Bacteroides fragilis.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=817;
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Thermoplasmataceae, Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 155;
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SEQUENCE 465 AA; 51450 MW; 74E47FAFF0C44B5A CRC64;
                                                                                                                                                 Last sequence update)
Last annotation update)
regulator.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical membrane protein.
OrderedLocusNames=Ta0679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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100.0%; Pred. No. 29;
tive 0; Mismatches
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100.0%; Pred. No. 11;
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                                                                                                               25-0CT-2004 (TrEMBLrel, 28, 25-0CT-2004 (TrEMBLrel, 28, 25-0CT-2004 (TrEMBLrel, 28, ABRC family transcriptional
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Best Local Similarity 100.9
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Matches 8; Conservative
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SEQUENCE FROM N.A.
STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
STRAIN=RI / ATCC 13939 / DSM 20539 / NOIB 9279;
MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonal L.A., Utterback T.R., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO.0016621; C:integral to membrane; IEA.
GO, GO.0016520; F:tetracycline:hydrogen antiporter activity; IEA.
GO, GO.0015520; F:tetracycline:hydrogen antiporter activity; IEA.
GO, GO.0015904; P:tetracycline transport; IEA.
GO; GO:0016904; P:transport; IEA.
InterPro; IPR004638; Efflux_EmrB.
InterPro; IPR00114; MFS.
InterPro; IPR00114; TCR_TetA.
InterPro; IPR001411; TCR_TetB.
InterPro; IPR001411; TCR_TetB.
InterPro; IPR001411; TCR_TetB.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 AA; 67778 MW; 4168A0998E467A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Score 8; DB 2;
100.0%; Pred. No. 39;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0711; efflux_EmrB; 1. PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  radioduranā Rl.";
Science 286:1571-1577(1999).
EMBL; AE001862; ARF12254.1; -.
PIR; G75599; G75599.
      Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01035; TCRTETA
PRINTS; PR01036; TCRTETB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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SEQUENCE 643 AA
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                          NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M.;
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Matches
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Buell C.R., Yuan Q., Ouyang S., Liu J., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                  Putative kelch-containing protein.

ORFNames=OSJNBa0073L01.3;

Oryas sativa (japonica cultivar-group).

Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.,
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AC092548, AAMM18732.1; --

EMBL, AE017083, AAPS53323.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Drug transport protein, putative.
OrderedLocusNames=DRA0061;
                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 30;
tive 0; Mismatches
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                                                                                                                                                                                                475 AA
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InterPro; IPR001810; F-box.
InterPro; IPR001682; Kelch rep.
Ffan; PF00646; F-box; 1.
Ffan; PF001344; Kelch 1; 2.
SWART; SW00612; Relch 1; 2.
SWART; SW00612; Relch; 2.
SWART; SR00612; Kelch; 2.
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                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 300:1566-1569(2003)
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Best Local Similarity 100.4
Then 8; Conservative
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                                                                                                                                                                                             PRELIMINARY;
|||||||||
412 VLIVIFTV 419
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gramene; Q8S6N3;
                                                                                                                                                                                                                              Q8S6N3;
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                                                                                                                                                                                             Q8S6N3
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109R293
AC 09R29
BT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DR Drug
GN Drug
GN Deino
OC Bacte
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10886N3
100836N3
100836N3
10070736
000 Spera
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Gaps

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Length 643; 0; Indels

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                                                                                                                                           CG1 protein.
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 8; DB 2; Length 939;
100.0%; Pred. No. 56;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP260819; AP469519; 1, --
InterPro; IRRO09011; Man6php recept.
SEQUENCE 939 AA; 109367 MW; EE96972DC096412D CRC64;
                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
  939 AA
PRT;
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Gape
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MEDLINE=97021710; PubMed=8868070;
Noutree A., Treacy G.B., Shaw D.C., Jeffrey P.D.;
Noutree A., Treacy G.B., Shaw D.C., Jeffrey P.D.;
Platypus insulin: indications from the amino acid sequence of significant differences in structure from porcine insulin.";
Biol. Chem. Hoppe-Seyler 377:147-153(1996).
Increases cell permeabllity to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

-- SUBNIT; Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewigs S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY060851; AAL28399.1; --
EMBL; AY060855; AAL28339.1; --
EMBL; AY060855; AAL28333.1; --
EMBL; AY060855; AAL28373.1; --
EMBL; AY060855; AAL46 MW; 432F8F340E895DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=INS;
Onithorhynchus anatinus (Duckbill platypus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
GM03003p (GM01206p).
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0277; INSULINB.
SMART; SM00078; I1GF; 1.
PROSITE; PS00262; INSULIN: 1.
Direct protein sequencing; Glucose metabolism; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
PIR; 863591, 863590.
PIR; PO1308; JMHJ.
InterPro; IPR004825; Ins/IGF/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9TQY7; Q9TQY8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-UL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 2;
Pred. No. 35;
0; Mismatches
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Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98054002; PubMed=9393853; DOI=10.1016/S0092-8674(00)80447-X; Su X., Kirkman L.A., Fujioka H., Wellems T.B.; "Complex polymorphisms in an approximately 330 kDa protein are linked to chloroguine resistent P. falciparum in Southeast Asia and Africa."; Cell 91:593-603(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AR44506; CAD50843.1;
InterPro; IPR009011; Man6php_recept.
SEQUENCE 1248 AA; 146629 MW; FDBE0EBFIDF769C2 CRC64;
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Name=PF07 0335,
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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STRAIN=HB3;
Su X.-Z., Kirkman L.A., Wellems T.E.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030690; AAC47851.1; -.
PIR; T09076; T09076.
InterPro; IPR009011; Man6php_recept.
SEQUENCE 950 AA; 110601 MW; ED19FEA3B517A378 CRC64;
                                                                                         Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches
                                            950 AA.
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100.0%; Pred. No. 72;
tive 0; Mismatches
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Q95NV2;
01-DEC-2001 (TrEMBLrel. 19, Created)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                            01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 100...
8; Conservative
                                            PRELIMINARY;
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1D Q81B28
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GN Name=
OX NCBI
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RESULT 16 Q95NV2 ID Q95NV AC Q95NV DT 01-DE

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MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797; MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797; MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swarzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dalle H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Groc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                  Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX245796; AAP04346.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 92;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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 74;
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                  Mismatches
 100.0%; Pred. No.
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ProDom; PD003679; Thioredoxin_like; 1.
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nes 7; Conservative
                  7; Conservative
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 Best Local Similarity
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                                                                                    19 QLRQLVR 25
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                                                                                                                                                                                                                                                              Sun4p (Fragment).
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01-JUN-2003 (
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SEQUENCE
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Q9HSN3;
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                  Matches
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MEDIINE=2225415; PubMed=12324359;
DOI=10.1128/AEM.68.10.5082-5095.2002;
BETTY C., O'Niel S., Ben-Dones A.F., Murphy L., Quail M.A. Harris D., Zaritsky A., Parkhill J.,
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Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
                                                                    0; Indels
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                                  Length 51;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1430;
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Appl. Environ. Microbiol. 68:5082-5095(2002).
EMBL; AL731825; CAD30135.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294142; CAD74279.1; -.
Complete protecome; Hypothetical protein.
SEQUENCE 73 AA; 8265 MW; EP2CS86B58F7443F CRC64;
 5854 MW; 0E4D30265D77EAA3 CRC64;
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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                                  2.5%; Score 7; DB 1;
100.0%; Pred. No. 45;
rative 0; Mismatches
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                                Score 7; I
Pred. No.
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                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=RB5505;
                                                                    Conservative
                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                        178 EKGFYYI 184
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                                              Local Similarity
nes 7; Conserv
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51 AA;
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 SEQUENCE
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RESULT 18
OTURO
AC 07URO
AC 07URO
DT 01-0C
DT 01-0C
DE HYPOT
GN Rhodo
OC Bacte
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RN RESEQUE
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**Q8KH11** 

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RESULT 19
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Gaps

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CARBOHYD
SEQUENCE
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Q97Y77
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STRAIN=306 / ATCC 13902 / XV 101;

STRAIN=306 / ATCC 13902 / XV 101;

MEDLINE=20202145; PubMed=12024217; DOI=10.1038/417459a;

MA G.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Forno J.A., Bartolini M.C., Camargo L.B.A.,

A Alves L.M.C., do Amaral A.M., Bartolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coulinho L.L., Cureino-Santos J.R., El-Dorry H.,

Formighiest E.F., Franco M.C., Grapel C.C., Furlor M.I.T.,

Formighiest E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinoda L.A.F., Tarkita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

"Tomparison of the genomes of two Xanthomonas pathogens with differing
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Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
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STRAIN=RH;
MEDLINE=91216437; PubMed=2022319; DOI=10.1016/0378-1119(91)90044-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Last annotation update)
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(Rel. 35, Last sequence update)
(Rel. 44, Last annotation update)
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                                      Mismatches
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100.0%; Pred. No. 78;
tive 0; Mismatches
Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                       Created)
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EMBL; AE011781; AAM36362.1; -.
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01-0CT-2002 (TrEMBLrel. 22, Ls
01-0CT-2002 (TrEMBLrel. 22, Ls
Hypothetical protein XAC1492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=XAC1492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 7; Conservative
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                                                                                               FVSVTNE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 NDRIFVS 259
                                                                                                                                                     13 FVSVTNE 19
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01-NOV-1997
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Q27001;
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Q8PMD7;
                                                                                                                                                                                                                                              RESULT 22
108 PMD
AC 08 PMD
AC 08 PMD
DT 01-0C
DT 01-0C
DT 01-0C
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DE HYPOT
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AH4 TOXGO
ID Q270T
AC Q270T
DT 01-NO
DT 01-NO
DT 05-JU
DE Antig
GN Name=
GN TOXOP
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MEDLINE-20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Johnson A.M., Illana S.; "Cloning of Toxoplasma gondii gene fragments encoding diagnostic antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 34 N-linked (GlcNAc. .) (Potential) 96 AA; 10853 MW; 69C7C2D14890FA53 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MXK3.
Arabidopsis thaliana (Mouse-ear cress)
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100.0%; Pred. No. 87;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 80;
iive 0; Mismatches 0; Indels
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SSO1462.
OrderedLocusNames=SSO1462;
Sulfolobus solfataricus.
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Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                  Gene 99:127-132(1991).
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Gaps

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Indels

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Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
Chain P., Lamerdin J.E., Regala W., Allen B.E., McCarren J.,
Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
BMBL; BSS69689; CAE06686.1;
Complete proteome; Hypothetical protein.
SEQUENCE 121 AA; 13842 MW; CE9C32B4C63B11F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Downrequlated in ovarian cancer 1-myosin-like protein (Fragment).
Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-22825697; PubMed=12917641; DOI=10.1038/nature01943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 121;
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laughlin A.M., Ing N.H.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX349169; AAQ24841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 123
123 AA; 13650 MW; 94B630F68B02FF3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Synechococcus sp. (strain WH8102).
Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 25, Last sequence update) (TrEMBLrel. 25, Last annotation update)
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0
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                                                                                                                                                                                                                                     121 AA.
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  0; Mismatches
                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                     (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=SYNW0353;
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  7; Conservative
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                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                      106 FTVLLOS 112
                                                     22 FTVLLOS 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 DPNDEES 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=84588;
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                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
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01-0CT-2003
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SEQUENCE
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     Matches
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                                                                                                                         STRAINE-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427736; DOI=10.1073/pnas.141222098;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Lan-Wehler C.C.-Y., Clausen I.G., Curtis B.A.,

A wayez M.J., Chan-Wehler G.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gassterland T.,

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Proc. Nall. Acad. Sci. U.S.A. 98:7835-7840(2001).

REMBL, AE006762; AAK41690.1;

RINE PIR, C90304; C90304.
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STRAIN=MUSO / ATCC 700699;

STRAIN=MUSO / ATCC 700699;

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cul L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome; Hypothetical protein.
SEQUENCE 107 AA; 12018 MW; 9471937E9819A836 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=truncated-res; OrderedLocusNames=SAVP030;
Staphylococcus aureus (strain Mu50 / ATCC 700699).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBL_TaxID=158878;
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100.0%; Pred. No. 92;
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GO; GO:0006310; P:DNA recombination; IEA.
InterPro; IPR006118; Recombinase_S.
InterPro; IPR006119; resolvase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5%; Score 7; DB 2
100.0%; Pred. No. 88;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003367; BAB47538.1; -. HSSP; P03012; 2RSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lancet 357:1225-1240(2001).
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SEQUENCE 112 AA; 12884 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04143; DUF395; 1.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                      SEQUENCE FROM N.A.
                                                NCBI_TaxID=2287;
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AC 0932M3
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AC 0932M
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0; Indels

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Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                  236 EYGLYSI 242
                                                                                                            81 EYGLYSI 87
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01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K1
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Q9YBC2;
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"Analysis of the genetic differences between Neisseria meningitidis and Neisseria genortheae: two.closely related bacteria expressing two different pathogenicities.";
Proc. Natl. Acad. Sci. U.S.A. 93:11109-11114(1996).
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                          STRAIN=Z2491;
MEDLINE=97008141; PubMed=8855317; DOI=10.1073/pnas.93.20.11109;
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                                                                                                         Neissēria meningitīdis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 7; DB 2; Length 125; 100.0%; Pred. No. 1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gardner A.E.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AA; 12834 MW; 92D8F57FD4493496 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
12-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein T02C12.4.
ORFNames=T02C12.4;
                    01-FEB-1997 (TrEMBLrel. 02, Created)
C1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Hemolysin A homolog (Fragment).
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EMBL; 238112; CAD36484.1; -.
EMBL; 235603; CAD36496.1; -.
EMBL; 238112; CAD36496.1; -.
WormBaes; WEGene00011369; T02C12.4.
WormPep; T02C12.4; CE30825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
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Best Local Similarity 10v...
7; Conservative
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                            NCBI_TaxID=487;
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NON TER
SEQUENCE
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SO DRA REPRETATION OF SECTION OF 
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DB 2; Length 134;

2.5%; Score 7;

Query Match

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STRAIN=Newman, and ISP479C;

STRAIN=22923846; PubMed=14563862;

MEDLINE=22923846; PubMed=14563862;

MEDLINE=2292316.278-6286.2003;

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J. Bacteriol. 185:6278-6286 (2003).

EMBL; AJ556794; CAD89109.1; -.

EMBL; AJ556795; CAD89113.1; -.
                                                                                                                                                                                                                                                                                                               MEDLINE-99310339; PubMed=10382966;
Kawarabayaai Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Jin-no K., Takahashi M., Sekine M., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Makamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
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                                                                                                                                                             Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6.83-101(1999).
EMBL; AP000062; BAA80676.1; -.
PIR; G72548; G72548.
Complete proteome; Hypothetical protein.
SEQUENCE 155 AA; 16841 MW; 1AA47C685D52939B CRC64;
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SEQUENCE 157 AA; 17665 MW; AP973D8D95D5963E CRC64;
                                                                  (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
  155 AA
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                                           01-NOV-1999 (TrEMBLrel. 12, Created)
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  PRT;
                                                                                                           Hypothetical protein APE1675.
OrderedLocusNames=APE1675;
                                                                                                                                                                                                        Desulfurococcaceae; Aeropyrum
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Best Local Similarity 100.
Matches 7; Conservative
PRELIMINARY;
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Created)
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Name=Tb927.1.4490;
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Les 7; Conservative
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90 ASFFGAF 96
                                                      Complete proteome.
SEQUENCE 157 AA;
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Q9N8D4
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                                                                                                                                                                                                                                                                                                                        PubMed=15213124; DOI=10.1073/pnas.0402521101;
Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth T., Chullingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Sharp S., Simmond M., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmond M., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15213324; DOI=10.1073/pnas.0402521101; S.J., Day N.P.J., PubMed=15213324; DOI=10.1073/pnas.0402521101; S.J., Day N.P.J., Holden M.T.G., Foster T.J., indexay J.A., Peacock S.J., Day N.P.J., Baright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Corton C., Cronin A., Doggett J., Dowd L., Chucher I., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Parkhill J.;
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evidence for the rapid evolution of virilence and drug resistance.";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
EMBL. BXS71857; CAG42448.1; -.
COMDLete protecome.
SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;
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2.5%; Score 7; DB 2; Length 157;
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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5.-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05.-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative membrane protein.
                                                                                                                                                                                                                                                      Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
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Bacteria: Firmicutes; Bacillales; Staphylococcus.
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Best Local Similarity luve.
7; Conservative
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             Best Local Similarity 100.
Matches 7; Conservative
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Q6GITS;
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A Bart-Delabesse E.N., Gerrare C.S., Atkin R.J., Barron A.J., Bowman S.,
Bary-Allen S.P., Bringaud F., Clark L.N., Corton A.J., Bowman S.,
A Bary-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
A Ray M.P., Leech V., Mayes R., Price C., Quail M.A., Rabbinowitch E.,
A Reiter C., Rutherford K., Sasse J., Sharp S., Shownkeen R.,
Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,
Barrell B., Malville S.E.,
"The DNA sequence of chromosome I of an African trypanosome: gene
Tronient, chromosome organisation, recombination and polymorphism.";
Nucleic Acids Res. 31:4664-4073 (2003).
R GO, GO:0008080; F.N-acetyltransferase activity; IEA.
GO, GO:0016740; F:transferase activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R InterPo; IPR000182; GCNSacetyl_trans.
R Fann, FP000583; Acetyltransf_l: 1.
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBL_TaxID=5691;
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"Complete genomes of two clinical Staphylococcus aureus strains: evidance for the rapid evolution of virulance and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
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NCBI_TaxID=184922;
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                                                                                                                                                                                    157 AA; 17665 MW; AF973D8D95D5963E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Gaps

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Query Match 2.5%; Score 7; DB 1; Length 193; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
       Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                      Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                  2.5%; Score 7; DB 2; Length 191; 100.0%; Pred. No. 1.5e+02; attive 0; Mismatches 0; Indels
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Complete protecome; Hypothetical protein.
SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;
                                                          preliminary data.
, AACB01000012; EAA42045.1; -.
ENCE 191 AA; 21255 MW; F1D7FEF8FFCC2A73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 417:459-463(2002).
-!- SIMILARITY: Belongs to the UPF0307 family.
                                                                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical UPF0307 protein XCC2605.
                                                                                                                                                                                                                 193 AA.
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InterPro; IPR006839; DUF615.
InterPro; IPR001232; Skp1.
InterPro; IPR008945; Skp1_Skp2.
Pfam; PF04751; DUF615; 1.
                                                                                                                                                                                                                                     05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE012372; AAM41877.1; -.
                                                                                                                                                                                                                                                                              OrderedLocusNames=XCC2605;
                                                                                       Query Match
Best Local Similarity luv...
7; Conservative
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A Salvea L.A. Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Radagilo R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A., Almeida N.F., Cardozo J., Chambergo F., Ciapina L.P., RA Cicarelli R.M.B., Franco M.C., Greggio C.C., Ferro M.I.T., RA Faria J.B., Franco M.C., Greggio C.C., Gruber A., Acaslyama A.M., Kishi L.T., Lette R.P., Lemos B.G.M., Lemos M.V.F., Acasli B.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M., Martine B.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., A Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., Tended Gos Santos M., Turiffi D., Teai S.M., White F.F., Tezza R.I.D., The Setubal J.C., Kitajima J.P., The Setubal J.C., Kitajima J.P., The Setubal J.C., Kitajima J.P., The Setubal J.C., Matalina J.P., The Setubal J.C., Matalina J.P., The Setubal J.C., Matalic M.J., Matalina J.P., The Setubal J.C., Matalina J.C., Matalina J.P., The Setubal J.C., Matalina J.P., The Setupa J.C., Matalina J.C., M
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001232; Skpl.
InterPro; IPR009945; Skpl_Skp2.
InterPro; IPR009945; Skpl_Skp2.
InterPro; IPR0016183; UCP016183; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 193 AA; 22033 MW; F3418B2AFAF98257 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 417:459-463(2002).
-1- SIMILARITY: Belongs to the UPF0307 family.
                                                                                                05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 45, Last annotation update)
Hypothetical UPF0307 protein XAC2766.
PRT; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 1.5 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00765; -; 1.
InterPro; IPR006839; DUF615.
                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=XAC2766
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Best Local Similarity 100.*
Matches 7; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=92829;
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05-JUL-2004 (Rel. 44, Last annotation update)
                                               Name=GMNN;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 185:2759-2773 (2003).

-!- FUNCTION: Catalyzes the transfer of the endogenously synthesized lipoate to apoproteins, creating an amide linkage that joins the free carboxyl group of lipoic acid to the epsilon-amino group of specific lysine residue in lipoate-dependent enzymes. Utilizes lipoyl-acyl-carrier protein as a source of lipoyl groups, although octanoyl groups from octanoyl acyl-acyl-carrier protein as a source of lipoyl groups, although octanoyl groups from octanoyl acyl-carrier protein (By similarity).

-!- CATALYTIC ACTIVITY: lipoyl-[acyl-carrier protein] + apo-protein = holo-protein + acyl-carrier protein.
-!- PATHWAY: Endogenous lipoate metabolism; lipoylation step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                               29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Lipoyltransferase (EC 2.3.1.-) (Lipoyl-(acyl-carrier protein)-N-lipoyltransferase) (Lipoylevin ligase B).
Name=lipB; OrderedLocusNames=NE1488;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=ATCC 19718 / IFO 14298;

MEDLINE=2256410; PubMed=12700255;

MEDLINE=2256410; PubMed=12700255;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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100.0%; Pred. No. 1.6e+02;
ve 0; Mismatches 0; Indels
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Prodom; PD006086; Lippate B; 1.
TIGRFAMs; TIGR00214; LipB; 1.
PROSITE; PS01313; LIPB; 1.
ACYLTANSFERSE; Complete proteome; Transferase.
SEQUENCE 204 AA; 22764 MW; AB3F6EF5F0346E61 CRC64;
                                                                     204 AA.
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GEMI_HUMAN
ID GEMI_HUMAN STANDARD; PRT; 209 AA.
AC 075496; Q9H1Z1;
DT 28-FEB-2003 (Rel. 41, Created)
jr 28-FEB-2003 (Rel. 41, Last sequence update)
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InterPro; IPR004143; BPL_LipA_LipB.
InterPro; IPR00544; Lipoate_B.
                                                                                                                                                                                                                                                                                                          Nitrosomonadaceae; Nitrosomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BX321861; CAD85399.1; -.
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                                                                   STANDARD;
                                                                                                                                                                                                                                                               Nitrosomonas europaea.
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les 7; Conserv
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                                                                LIPB NITEU
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Matches
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TISSUBELLUNG, and Urinary bladder;

TISSUBELLUNG, and Urinary bladder;

MEDLINE=2238257; PubMed=1247932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B. Buetow K.H., Schamfer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B. Buetow K.H., Schamfer C.F., Bhat N.K.,

Hopkins R.F., Mordan H., Moore T., Max S.I., Wang J., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Morlay D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDIAGE-9635433; DOI=10.1016/S0092-8674(00)81209-X; MEDLINE-9829736; PubMed=9635433; DOI=10.1016/S0092-8674(00)81209-X; MGGAITY, T.J., Kirschner M.W.; Replication, is degraded during "Geminin, an inhibitor of DNA replication, is degraded during
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:000050; P:cell cycle arrest; TAS. GO:000050; P:cell cycle arrest; TAS. InterPro; IPR009984; Geminin. Pfam; PP07412; Geminin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corby N.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the geminin family.
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EMBL; AL133264; CAC3151.1; ALT_INIT.
EMBL; BC005185; AAH05188.1; -.
EMBL; BC005389; AAH05389.1; -.
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Genew; HGNC:17493; GMNN.
H-InvDB; HIX0005629; -.
                                                                                                                                                                                                                                                                                                                                                   mitosis.";
Cell 93:1043-1053(1998).
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                                                                                                                      WCBI_TaxID=9606;
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Gaps
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genomic Bequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005939; BAC46479.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio vulnificus (strain YJO16).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.5%; Score 7; DB 2; Length 220; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      Query Match 2.5%; Score 7; DB 2; Length 220; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                       220 AA; 23104 MW; 45AC3A0F411769FE CRC64;
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SEQUENCE 220 AA; 23332 MW; 0AD03221F4C1A350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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EMBL; AY463186; AAS19962.1; -.
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR005834; Dehal Ilke_hydro.
Pfam; PF00702; Hydrolase; I.
PROSITE; PS00154; ATPASE_E1_E2; UNGNOWN_1.
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01-MAR-2004 (TrEMBLrel. 26, Last seg
01-MAR-2004 (TrEMBLrel. 26, Last ann
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OrderedLocusNames=blr1214;
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| 126 ELVIHEK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=USDA110;
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01-JUN-2003 (
01-JUN-2003 (
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SEQUENCE
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Q89V44
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     REREEFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
HR-like lesion-inducing protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB025608; BAA95731.1; -.
InterPro; IPR018637; HR lesion.
InterPro; IPR011592; Surf4_rel.
Propom; PD010195; Surf4_rel.
Propom; PD010195; Surf4_rel.
Propom; P2010195; Surf4_rel.
SEQUENCE 217 AA; 252I9 MW; F88CDE1A0BEABC4F CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae; Acidovorax.
                                                 Query Match 2.5%; Score 7; DB 1; Length 209; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
  23565 MW; OBABE60F6F5AC252 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
2.5%; Score 7; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0;
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Appl. Environ. Microbiol. 70:1698-1707(2004).
                                                                                                                                                                                                                                                                                                                                                 217 AA
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MEDLINE=20277480; PubMed=10819329;
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                            193 QEEIKEN 199
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  209 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-B0447
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  SEQUENCE
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Toxoplasma gondii.
Eukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida, Sarcocystidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BK;
MEDLINE=20542029; PubMed=11087916; DOI=10.1016/S0166-6851(00)00296-6;
BRDLINE=20542029; PubMed=11087916; DOI=10.1016/S0166-6851(00)00296-6;
Brydges S.D., Sherman G.D., Nockemann S., Loyens A., Daubener W.,
Dubremetz J.F., Curruthers V.B.;
"Molecular characterization of TgMICS, a proteolytically processed antigen secreted from the micronemes of Toxoplasma gondii.";
Mol. Blochem. Parasitol. 11:51-66(2000).
EMBL; Y09782; CAA70921.1; -..
EMBL; Y09782; CAA70921.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 231;
0. 1.8e+02;
ches 0; Indels
                                                                                                    2.5%; Score 7; DB 2; Length 230;
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
EMBL; AAABO1008987; EAAO1660.1; -.
SEQUENCE 232 AA; 25104 MW; COC96A97FB332E0B CRC64;
                                                                     230 AA; 24443 MW; 189C4651DAE35A72 CRC64;
                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=agCG47164; ORFNames=ENSANGG0000006384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 AA.
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100.0%; Pred. No. 1.8
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Created)
   GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-DEC-2001 (TrEMBLrel. 19,
            InterPro; IPR007300; LrgB.
Pfam; PF04172; LrgB; 1.
Complete proteome.
SEQUENCE 230 AA; 24443
                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                          20 VIFTVLL 26
                                                                                                                                                                                             11 VIETVLL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5811;
                                                                                                                                                                                                                                                                                                                                                                                    H4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxoplasma.
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                                                                                                       Query Match
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P90611
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Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.; The genome sequence of Bacillus creus ATCC 10997 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOl."; Nuclei, AE017280; AAS44136.1; -.
                                                                                                                                                                          Gaps
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Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.; "Comparative genome analysis of Vibrio vulnificus, a marine pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio vulnificus.
Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
                                                                                                                                      Score 7; DB 2; Length 222;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5%; Score 7; DB 2; Length 222; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016797; AA008706.1; -.
Complete proteome.
SEQUENCE 222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                    EMBL, AP005334; BAC93785.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q72XY8;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Membrane protein, putative.
OrderedLocusNames=BCE5235;
                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Uncharacterized protein conserved in bacteria
                                                                                                                                                                                                                                                                                                                                  222 AA.
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                                                                                                                                      Query Match 2.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                   Genome Res. 13:2577-2587(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=VV10168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrionaceae; Vibrio.
NCBI_TaxID=672;
                                                                                                                                                                                                            246 GIFELKE 252
                                                                                                                                                                                                                                            190 GIFELKE 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                  Q8DFN8
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15006795; DOI=10.1128/AEM.70.3.1698-1707.2004; Coombs J.M., Barkay T.; "Molecular evidence for the evolution of metal homeostasis genes lateral gene transfer in bacteria from the deep terrestrial
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                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 AA; 24249 MW; F85D924477FB916F CRC64;
                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
  100.0%; Pred. No. 1.8e+02; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appl. Environ. Microbiol. 70:1698-1707(2004).

EMBL, AY463173; AAS19949:1; -..

GO; GO:00038152; F:catalytic activity; IEA.

GO; GO:0008152; F:catalytic activity; IEA.

InterPro; IPR001757; ATPase E1-E2.

InterPro; IPR001259; B1-E2_ATPase-reg.

PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
                                                                                                                                                                                                                                                                          232 AA
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SEQUENCE FROM N.A.
MEDLINE=91110576; Pubmed=1703303;
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MEDLINE=88111517; PubMed=3501369;
                                                                                                                                                                                                                                                                                                                                                                                                               PIB-type ATPase (Fragment).
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                               7; Conservative
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EMBO J. 6:3313-3316(1987)
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                                                                                  TVLLQSL 29
                                                                                                                                  TVLLOSL 52
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subsurface.";
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0658B3
1D 065B3
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00 07 JT
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CD7 HUMAN
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DT 01-MA
DT 01-MA
DT 01-MA
DT 05-UI
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CTISSUB-Muscle;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WE Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Districtench C., Marusina K.W., Farmer A.A., Rubin G.M., Hong L.,

Rahas S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Boask S.A., McEwan R.J., McKernan K.J., Male K.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radarguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse chan a second of the seco
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Schanberg L.E., Fleenor D.E., Kurtzberg J., Haynes B.F., Kaufman R.E.; "Isolation and characterization of the genomic human CD7 gene: structural similarity with the murine Thy-1 gene."; Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).
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MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;
Lyman S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.;
"Identification of CD7 as a cognate of the human K12 (SECTM1)
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MEDLINE=91267564; Pubmed=1711009;
Yoshikawa K., Seto M., Ueda R., Obata Y., Notake K., Yokochi '
Takahashi T.;
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    J. Biol. Chem. 275:3431-3437 (2000).
    PENOCTION: Not yet Known.
    SUBINIT: Interacts with SECTMI.
    SUBILILIALAR LOCATION: Type I membrane protein.
    SUBILIARITY: Contains 1 immunoglobulin-like domain.
    DATABASE: NAME-PROW; NOTE=CD guide CD? entry;
    WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd7.htm".

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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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InterPro; IPR010166; Staph reg_Sar.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
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                                                                                                                                         Q9EZK4;
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 357:1225-1240(2001)
           Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                      Rot-like protein Rlp.
                                                     169 LRNGELV 175
                                                                          101 LRNGELV 107
                                                                                                                                                                                                                                                                                                                                                                                                          255 RIFVSVT 261
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                                                                                                                                                                                               Name=rlp;
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Q99RD5;
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                                                                                                                               Q9EZK4
                                                                                                           RESULT 52
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                                                 GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005886; C:membrane fraction; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004972; F:receptor activity; TAS.
GO; GO:00042110; P:T-ceptor activity; TAS.
GO; GO:00042110; P:T-cell activation; TAS.
GO; GO:000169; P:transmembrane receptor protein tyrosine kin. .; NAS.
InterPro; IPR003599; IG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=YCH46;
Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
Kuwahara S., Hattori M., Hayashi T., Ohnishi Y.;
"Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
EMBL; AP006642; BAD51354.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 240 AA; 27646 MW; DCICF4292674BEP8 CRC64;
                                                                                                                                                                                                                                                                                      4 X 9 AA tandem repeats, potential spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                   PEGM, PF00047; ig; 1.
SWART; SW00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
Antigen; Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Receptor; Repeat; Signal; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 7; DB 1; Length 240;
100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                              T-cell antigen CD7.
Extracellular (Probable).
Probable.
                                                                                                                                                                                                                                                                                                                                                                                                          25409 MW; EBBCE08279552108 CRC64;
                                                                                                                                                                                                                                                                                                                             S-palmitoyl cysteine.
N-linked (GloNAc. .)
N-linked (GloNAc. .)
                                                                                                                                                                                                                                                                Cytoplasmic (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA
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Best Local Similarity 100.0%; Pred. No. 1.0
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                           Potential.
                                                                                                                                                                                                                                                                                                                      Potential
                                                                                                                                                                                                                                                                                                function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                               H-InvDB; HIX0014252; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
ORFNames=BFp0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteroides fragilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 NTLSSPN 140
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 PIR; A39016; A39016.
           HSSP; P01607; 1BWW.
Genew; HGNC:1695; Cl
                                                                                                                                                                                                                                                                                                                                                                                                           240 AA;
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                                                                                                                                                                                                            fransmembrane.
                                          MIM; 186820;
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TRANSMEM
DOMAIN
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LIPID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                          DISULFID
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REPEAT
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SEQUENCE FROM N.A.
STRAIN=MUSO / ATCC 700699;
MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K. Staphylococcus
                                                          Gaps
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Length 240;
                                                          0; Indels
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MCNamara P.J., Milligan-Monroe K., Proctor R.A.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288198; AAG45334.2; -.
HSSP, Q53777; 1F2P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR010166; Staph reg_Sar.
InterPro; IPR009058; Wing hix DNA bnd.
TIGRFAMs; TIGRO1889; Staph reg_Str; 2.
SEQUENCE 247 AA; 29792 mW; D0783668666082B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Olimniano (Tremblrel. 17, Last sequence update)
Olimna.2001 (Tremblrel. 26, Last sequence update)
Olimniano (Tremblrel. 26, Last annotation update)
Staphylococcal accessory regulator A homolog.
Name-sarkli, orderedlocusmanes-SAV2499;
Staphylococcus aureus (strain Muso / ATCC 700699).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Staphylococcus
NCBI_TaxID=1280;
DB 2; Le
o. 1.8e+02;
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2.5%; Score 7; DB 2
100.0%; Pred. No. 1.8
tive 0; Mismatches
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aureus.";
Lancet 357:1225-1240(2001).
EMBL; AP003137; BAB43590.1; -.
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SEOUENCE 247 AA
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094262
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MEDLINE-21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; MEDLINE-21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Yabawa H., Kobayamah I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizukama H., Kawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanamori M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Yoshino C., Shiba T., "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iamana N., Abano K., Naimi T., Kuroda H., Cui L., Kamamoto K., Hiramatsu K., Ramanatsu K., Rishamatsu K., Alamanatsu K., Remena and virulence determinants of high virulence community-
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                                                                                              Query Match 2.5%; Score 7; DB 2; Length 247; Best Local Similarity 100 0%; Pred. No. 1.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 7; DB 2; Length 247; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
                      Complete proteome.
SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus (strain N315).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=sarH2; OrderedLocusNames=MW2418;
Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                      247 AA
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InterPro, IPR010166; Staph reg Sar.
InterPro, IPR009058; Wing hlx DNA bnd.
TIGRFAMS; TIGR01889; Staph_reg_Sar; 2.
TIGRFAM8; TIGR01889; Staph_reg_Sar; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=sarH2; OrderedLocusNames=SA2287;
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                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                              255 RIFVSVT 261
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91 RIFVSVT 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acquired MRSA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SarH2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                             Q7A004;
05-JUL-2004
05-JUL-2004
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O7A004
O AC O7A00
DT O5-JT
DT
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                                                                                                                                                                                                                                                                                                                      DB 2; Length 247;
                                                                                                                                                                                                                                                                                                            Query Match 2.5%; Score 7; DB 2; Length 247; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                             247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SPBPBB7.13 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative staphylococcal accessory regulator OrderedLocusNames=SAS2385;
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InterPro; IRR010166; Staph reg_Sar.
InterPro; IRR010166; Staph reg_Sar.
IIGRFAMs; TIGREAMs; TIGREAMs; TIGREAMs; 247 AA; 29793 MW; 90ARTRO
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QGGH6;
05-JUL-2004 (TrEMBLrel. 27, Created)
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Best Local Similarity 100...
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Pfam; PF00990; GGDEF; 1.
SMAART; SM00267; DUF; 1.
TIGRFAM#; TIGR00264; GGDEF; 1.
PROSITE; PSS0887; GGDEF; 1.
                                                                                                                                                                                                    Query Match
Best Local Similarity 100.º
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                          275 FGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                 168 FGAFLVG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 RPQEEIK 176
                                                                                                                   Complete proteome. SEQUENCE 253 AA;
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061671
AC 06367
DT 25-0C
DT 25-0C
DT 25-0C
DF Hydro
DE Hydro
OX NCBI-
RN (1)
RP SEQUE
RA Hitch
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                                                                                                                                                          RA WOOD V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ray Wood V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bourons J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Sgouros J., Pater N., Hayles J., Baker S., Basham D., Bowman S., Ra Gollins M., Connor R., Cronin A., Davis D., Helwell T., Fraser A., Collins M., Connor R., Cronin A., Davis D., Helwell T., Fraser A., Racollins M., Connor R., Hamlin N., Harris D., Hadago J., Hodgson G., R. Horropd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., R., James K., James K., James M., Lones M., Leather S., McDonald S., McLean J., R. Anders M., Mungall K., Murphy L., Niblett D., Odell C., R. Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rak Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., R. Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S., Raltor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S., Rablor K., Taylor R.G., Art R., Robben J., Gyrmonprez B., Meltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., Rak Hilbert H., Borzaym K., Langer I., Back A., Lehrach H., Wambutt R., Purnelle B., R. Gobel C., Fuchs M., Dusterhoff A., Fritzc C., Holzer E., Moter R., Murse S., Lelaure V., Mottier S., R. Gabel C., Fuch M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Boninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., R. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., R. Marue 415:871-88012002)

R. Rebl, ALO32684; CAA217081; J. R. Rebl, Roche B., Rebband B., Barrell B.G., Nurse P., Rebband B., Rebband B., Barrell B., Rebband 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                 MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 7; DB 2; Length 251; ilarity 100.0%; Pred. No. 1.9e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenedB SPombe; SPBP8B7.13; -.
SEQUENCE 251 AA; 27746 MW; C631E344FDC0D686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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OrderedLocusNames=ml14839;
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DNA Res. 7:331-338(2000).
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   Schizosaccharomyces.
NCBL_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 DPNDEES 72
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MAFF303099;
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                                                                                       SEQUENCE FROM N.A.
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Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the BMBL/GenBank/DDBJ databases.
EMBL; CP000001; AAU16762.1; -.
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STRAIN=Ames / isolate Porton;
MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
Mead T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wn. M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
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                                                              2.5%; Score 7; DB 2; Length 253; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.5%; Score 7; DB 2; Length 271; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus ZK.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus anthracis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 AA; 31281 MW; 85C92D54129184BE CRC64;
253 AA; 27656 MW; 358A4F06B9B66C8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hydrolase, alpha/beta fold family (EC 3.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q81WUO; Q6HUZ3; Q6KP68;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hydrolase, alpha/beta fold family.
OrderedLocusNames=BA3877, BAS3592, GBAA3877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 AA.
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Gaps

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DB 2; Le... Mo. 26+02; 0; Indels

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8E6769086609B7F3 CRC64;
                                          2.5%; Score 7; DB 2
100.0%; Pred. No. 2e+
tive 0; Mismatches
       Complete proteome.
SEQUENCE 271 AA; 31382 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AA; 33723 MW;
                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                               BC026645 protein (Fragment)
Name=BC026645;
                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
1es 7; Conservative
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                             191 RFQEEIK 197
                                                                                                                   170 RFÓEBÍK 176
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                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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LGT_CHLCV
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                                                                                                                   Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H.; Longmire J., Lucas S., Okinaka R., Suchates genome sequence of Bacillus thuringiensis 97-27."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AE017355, AAT60562.1; GO, GO: 0016787; P: Hydrolase activity; IEA. GO, GO: 0016787; P: Hydrolase activity; IEA. InterPro; IPR000073; A/b hydrolase. InterPro; IPR0003089; AB hydrolase. InterPro; IPR0003089; AB hydrolase. InterPro; IPR0003089; Ser estre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Koletce A.-B., Fraser C.M.; "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 271;
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2e+02;
... 0; Indels
                                                                                                                                                        "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AA; 31338 MW; D01E8F4D025FF187 CRC64;
                                                                                                                                                                                                                                                                                                                   TIGR; GBA3877; -.
GO: GO: 0016787; F: hydrolase activity; IEA.
GO: GO: 0016725; P: aromatic compound metabolism; IEA.
GO: GO: 0006725; P: aromatic compound metabolism; IEA.
InterPro: IPR000073; A/b hydrolase.
InterPro: IPR0031099; AB hydrolase.
InterPro: IPR0031099; SE_GETE.
PERN; PR00561; Abhydrolase.1; I.
PRINTS; PR00111; ABHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hydrolase, alpha/beta_fold_family (EC 3.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 20+
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=BT9727_3492;
Bacillus thuringiensis (Subsp. konkukian).
                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Hydrolase.
SEQUENCE 271 AA; 31338 MW
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                                                                                        SEQUENCE FROM N.A.
STRAIN-Ames / isolate 0581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                   Nature 423:81-86(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 RFQEEIK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 RFQEEIK 197
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WEDINES-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Nogin T.B., Toshlywis S., Carnina D., Mullahy S.J.,

B Nomberin M.J., Ubdin T.B., Toshlywis S., Carnina P.H.,

Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley N., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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100.0%; Pred. No. 2.2e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO26645; AAH36645.1; -.
MGD; MGI:2446129; BC026645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642B913C78884195 CRC64;
                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
293 AA.
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                                                                                  Created)
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Q823E7;
05-JUL-2004 (Rel. 44, Created)
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NCBI_TaxID=216466;
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Complete proteome.
SEQUENCE 298 AA;
                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Q6KZP1;
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ID Q6
AC Q6
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     OCC OXX SERVICE SERVIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Lipoprotein biosynthesis; first step.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                 MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321; Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., Heldelberg J.F., Holtzapple E.K., Khouri H.M., Federova N.B., Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M., Fraser C.M.; Genes and Golden Gold
                                                                               Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
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  05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annocation update)
Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-).
Name=lgt; OrderedLocusNames=CCA00471;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1E148CA397939E64 CRC64;
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Last annotation update)
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-!- SIMILARITY: Belongs to the lgt family.
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Potential
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Potential
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R HAMAP; MF 01147; -; 1.

R InterPror; IFRO01640; LGT.

R Pfam; PF01790; LGT; 1.

R PROSITE; PS01311; LGT; FALSE NEG.

COMOLETE PRO1311; LGT; FALSE NEG.

TRANSMEM 69

TRANSMEM 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 7; Conservative
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91
159
216
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137
194
223
260
296 AA;
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Probable)
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TRANSMEM
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08DXW4
10 Q8DXW
AC Q8DXW
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DT 01-MA
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STRAIN=2603 V/R / Serotype V;
MEDLINE=22222986; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222986; PubMed=12200547; DOI=10.1073/pnas.182380799;
Masignani V., Ciealewicz M.J., Eisen J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewiß M.R.,
Radune D., Pedorova W.B., Scanlan D., Khouri H.M., Mulligan S.,
Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
Fraser C.M.,
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MEDLINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
MEDGER P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
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100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein gbs1776.
OrderedLocusNames=gbs1776;
Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5%; Score 7; DB 2; Lei
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 AA.
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Mol. Microbiol. 45:1499-1513(2002).
BMBL: AL766853; CAD47435.1; -.
Sagalist; gbs1776; -..
Complete proteome.
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Matches 7; Conservative
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Best Local Similarity
7; Conserva
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PRT;
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EMBL; BT007042; AAP35691.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
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                                                                                                             122 VAAHITG 128
                                                                                                                                                  137 VAAHITG 143
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Q9VI33
ID Q9VI33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=P0627E03.4; Synonyms=OJ1288 G09.26;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eppermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: Belongs to the annexin family.
EMBL; AP005012; BAD17230.1; --
HSSP; P12429; JAXN.
HSSP; P12429; JAXN.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
InterPro: IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                        EMBL, AEGA. Sci. U.S.A. 101:9091-9096 (2004).

EMBL, AE017261, AAT31811.1;

GO: GO:0004347; F:glucose-6-plosphate isomerase activity; IEA.

GO: GO:0016853, F:isomerase activity, IEA.

GO: GO:0005529; F:sugar binding; IEA.

GO: GO:0005529; F:sugar binding; IEA.

InterPro: IPR001477; SIS.

Pfam; PF01380; SIS; 1.
                                                                                                                        Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Picrophilaceae; Picrophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 305; 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Isomerase.
SEQUENCE 305 AA; 35516 MW; 405D8A6001AC86CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA; 35554 MW; 1BF535BDBFD4A1F2 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Glucose/mannose-6-phosphate isomerase (EC 5.3.1.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                 STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674; DOI=10.1073/pnas.0401356101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD000143; Annexin; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                             Picrophilus torridus.
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Best Local Similarity
7; Conserva
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                                                                                                                                                                      NCBI_TaxID=82076;
                                                                                                                                                                                                              SEQUENCE FROM N.A
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SEQUENCE
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0626A7;
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10626A
AC 0626A
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AC 0626A
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**RIJORDER R.D., Colline F.S., Wagner L.H., Derge J.G.,

**RIJORDER R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

**Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Loquellano M.Y., Usdin T.B., Tooshiyuki S., Carrinci P., Frange C.,

**Rehar S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Villalon D.K., Muzny D.M., Sodergren E.J., Lu.X., Gibbs R.A.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Richards W.W., Touchman J.W., Green E.D., Dickson M.C.,

**Richards M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Richards M.M., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Richards M.M., Madan A., Woung A.C., Shevchenko Y., Bouffard G.G.,

**Richards M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Richards M.M., Madan A., Woung A.C., Shevchenko Y., Bouffard G.G.,

**Richards M.M., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Richards M.M., Madan A., Woung A.C., Shevchenko Y., Bouffard G.G.,

**Richards M.M., Touchman J.W., Green E.D., Dickson M.C.,

**Richards M.M., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Richards M.M., Madan A., Woung A.C., Shevchenko W., Schnerch A., Schein J.E.,

**Richards M.M., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Richards M.M., Madan A., Woung A.C., Shevchenko W., Schnerch A., Schein J.E.,

**Richards M.M., Stalska U., Smailus D.G., Schnerch A., Schnerch A., Schein J.E.,

**Richards M.M., Stalska U., Smailus G.G., Shevchenko W.C.,

**Richards M.M., Stalska U., Smailus G.G., Shevchenko W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLRel. 27, Last annotation update)
CREBLI protein (CAMP responsive element binding protein-like 1).
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            Length 314;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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Query Match
2.5%; Score 7; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0;
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REQUENCE FROM N.A.

Adams M.D. Celnikers S.E., Holt R.A., Evans C.A., Gocapne J.D.,

Adams M.D. Celnikers S.E., Holt R.A., Evans C.A., Gocapne J.D.,

Adams M.D. Celnikers S.E., Holt R.A., Evans C.A., Gocapne J.D.,

B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutcon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,

R. Brandon R.C., Benter E.G., Helf G., Nolson C.R., Baldwin D.,

Ballew R.M., Bencs P.V., Berman B.P., Bhandari D., Bolahakov S.,

Benkova D., Botchen M.R., Bouck J., Brokstein P., Brothier P.,

R. Benson K.Y. Bencs P.V., Berman B.P., Brandari D., Bolahakov S.,

Berkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,

R. Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,

Burlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

R. Bobson K., Doup L.E., Downes M., Dugalt-Rocha S., Dunkov B.C., Dunn P.,

R. Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Plaison B.C.,

R. Houston K.J., Brokstein D., Bw. I., Dietz S.M.,

Botton M., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,

R. Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

R. Mount S.M., Moyn W. B., Murphy L., Murzhy L., Morshrefi A.,

R. Bazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V., Rese M.G.,

Shue B.C., Stoan-Kiamos I., Simpson M., Stupski M.P., Smith H.O.,

R. Shiekas R., Zhodira C., Turner R., Vennison J.,

Shue B.C., Shord M., Weinschor K., Weinsenbach J.,

Shue S., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

R. Wang Z.Y., Wassarman D.A., Weinscock G.M., Weissenbach J.,

R. Wang Z.Y., Wassarman D.A., Weinscock G.M., Weissenbach J.,

R. Whore S. Shang W., Zhon M., Zhon S., Pollard S., Shue B.C., Shord W.,

R. Where S., Shord M., Weinscock G.M., W
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MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson E.J., Society J.M., Park S., Feiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI TaxDe7227,
                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel.'28, Last annotation update)
CG2336-PA (AT02555p).
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                    I_TaxID=7227;
                                                                                                                                                      ORFNames=CG2336;
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a genomics perspective."; Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

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MEDINE=22426069; PubMed=12537572;
Mistra S., Crosby M., Mungall G.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Calniker S.E., de Grey A.D., Drygdalle R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.C.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                           Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
NCBI_TaxID=2371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; DB 2; Length 322;
Pred. No. 2.4e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0037455; CG2336.
InterPro; IPR009961; DUF1487.
PEdm; PF07368; DUF1487; 1.
SEQUENCE 3122 AA; 36891 MW; D8680A7A63BB5988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Best Local Similarity 100.0%; Pred. No. 2.4
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
OrderedLocusNames=Xf0992;
Xylella fastidiosa.
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SEQUENCE FROM N.A.
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Celniker S.;
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01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2003 (TrEMBLrel. 24, Hypothetical protein CT839. OrderedLocusNames=CT839;
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Science 282:754-759(1998)
                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; NAD SEQUENCE 343 AA; 383
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       132 RSNTLSS 138
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                                    46 RSNTLSS 52
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                                                                                                            Q7VJZ3
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Matches
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                                                                                               27VJZ3
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A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Lemos E.G., Lemos M.V.; Lopes C.R., Madrido J.A., Lenos M.V.; Lopes C.R., Madrido J.A., Machado M.A., Madrira A.M.B., Madrira H.M.F., Marino C.L., Marques M.V., Martino E.M., Martino E.M.; Martino E.M.; Martino C.B., Mayaki C.Y., Montelaro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhoni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Pesquero J.B., Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Peroira G.A.G., Peroira R.C., Palmieri D.A., Paris A., Peroto B.R., Peroira G.A.G., Rodrigues V., de Rosa A.J.M., Peroto B.R., Peroira G.A.G., Rodrigues V., de Rosa A.J.M., A G. Slova V.E. Jr., de Salva A.G., Sancelli R.V., Sawasaki H.E., A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr., Peroira G. Silva A.C., de Silva A.M., A Salva M.A., Zatz M., Meidanis J., Squeira W.J., de Souza A.A., Vallada H., Van Sluys M.A., Verforeki D., Tere S. M., Truffi D., Tsai S.M., Tsubako M.H., Zago M.A., Zatz M., Meidanis J., Setubal J.C.; The Genome sequence of the plant pathogen Xylella fastidiosa."; Neurre 406:151-1591(2000).
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MEDLINE-99120557; PubMed=9923682; DOI=10.1038/16495;
MAID R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ADP-L-GLYCERO-D-MANNOHEPTOSE-6-EPIMERASE.
Name=gmhD; OrderedLocusNames=JHP0793;
Helicobacterr pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
(1)
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                     GO: 00:0003824; F: Catalytic activity; IEA.
InterPro; IPR000379; Ser estrs.
Complete proteome; Hypothetical protein.
SEQUENCE 327 AA; 35553 MW; 96A5841EBIA08E90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 AA; 37351 MW; DD1003F6A8C7A720 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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                                                                                                                                                                                                                                                                                             EMBL; AE003937; AAF83802.1; -.
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Matches 7; Conservative
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SEQUENCE 329 AA
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SEQUENCE FROM N.A.
STRAINED / UW-3 / Cx;
STRAINED / UW-3 / Cx;
MEDLINE=990000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Atchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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EMBL, AE017141, AAP7669611; -.
                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 51449 / 3B1;
MEDLINE=22709201; Pubmed=12810954; DOI=10.1073/pnas.1332093100;
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GO; GO:0008460; F:dTDP-glucose 4,6-dehydratase activity; IEA.
GO; GO:0009225; P:uclocide-eugar metabolism; IEA.
InterPro; IPR005889; dTDP_gluc_dehyt.
InterPro; IPR005899; Epimerase_Dh.
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 AA; 38920 MW; B528F6F2710A40D2 CRC64;
                             QYVJZ3;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DTDP-D-glucose 4,6-dehydratase (EC 4.2.1.46).
OrderedLocusNames-HH0099;
Helicobacter hepaticus.
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Last annotation update)
343 AA
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TIGRFAMs; TIGR01181; dTDP_gluc_dehyt; 1.
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PRT;
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NCBI_TaxID=32025;
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Search completed: June 22, 2005, 06:51:54
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MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
Mead T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J.D., Utterback T.R., Berry K.J.,
Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 28, Last annotation update)
05-DOCT-2004 (TrEMBLrel. 28, Last annotation update)
Name=OSTATC, Synonyms=B1080D07.14;
Name=OSTATC, Synonyms=B1080D07.14;
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermacophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                              DB 2; Length 354;
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100.0%; Pred. No. 2.6e+02;
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GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR005495; YigP_XigO.
InterPro; IPR039; YigP_XigO; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 354 AA; 40145 MW; E6A1317A124C10D1 CRC64;
                                                                                                                                                   354 AA; 40065 MW; AD79C8F2CD59F4E5 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein TC0227.
OrderedLocusNames=TC0227;
EMBL, AE001356, AAC68436.1; -.
PIR, G71465, G71465, G71465.
InterPro, IPR005495, YjgP_YjgQ.
Pfam, PF03739, YjgP_YjgQ.
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100.0%; Pred. No. 2.6
tive 0; Mismatches
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Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                            Complete proteome.
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                                                                                                                                                SEQUENCE
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Q9AVE6
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PEQUENCE FROM N.A.

PubMed=1244438; DOI=10.1038/nature01184;
Rasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Kanmori H., An J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanmori H., An Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., A. Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., A. Hijishita S., Honda M., Ichh Y., Itoh Y., Iwabuchi A., Kamiya K., A. Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., An Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamura M., Nagasaki H., Nakashima M., Nakama Y., Nakamuchi Y., Nakamura M., Nagasaki M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Imama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., The Genome sequence and structure of rice chromosome I.",
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[1]
SEQUENCE FROM N.A.
MEDLINE=21140310; PubMed=11244106; DOI=10.1104/pp.125.3.1248;
Agrawal G.K., Yamazaki M., Kobayashi M., Hirochika R., Miyao A.,
Hirochika H.;
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InterPrc; PR002031; Translocase.
Pfam; PP00902; TatC; 1...
PRINTS; PR01840; TATCFAMILY.
TIGREAMs; TIGR00945; tatC; 1...
PROSITE; PS01218; TATC; 1...
SEQUENCE 359 AA; 38763 MW; D253
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Matches 281; Conservative
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Adb61490 Human Apo
Adb61477 Human Apo
                                                                                                                                                                                                                                                                                                                                                                                                          Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.
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note= "putative N-linked glycosylation site"
114. .281
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/label= Extracellular_region
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|label= Transmembrane_region
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|Tabel= Cytoplasmic_region
                                                                                                ALIGNMENTS
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  ADB61490
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/note= "Claim 4"
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note= "Claim 3"
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                                                                                                                                             DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                              1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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Indels
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Mismatches
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(IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                 Similarity
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                                                                                                                              DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                        RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                            FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                               FYY IYSQTYFRFQEEIKENTKNDKQMVQY IYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                  Gaps
used for treating cachexia, cerebral madaria, rheumatoid arthritis osteoporosis, for preventing graft-host rejection, and as anti-inflammatory agents, for treating endotoxic shock or to prevent activation of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109. .111
/notes "potential N-glycosylation site"
149. .150
/notes "potential KEX2 protease processing site"
                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor related apoptosis inducing ligand; TRAIL; cytokine; cancer; leukaemia; lyphoma; melanoma; viral infection; thrombotic microangioplasty; therapy.
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                                                                              100.0%; Score 281; DB 2; Length 281; 100.0%; Pred. No. 2.9e-266; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "contains a receptor-binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "potential KEX2 protease processing
                                                                                                                                                                                                                                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                              SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19. .38
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39. .281
/label= Extracelular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .18
/label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                       Human apoptosis inducer cytokine TRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   AAW19787 standard; protein; 281 AA
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95US-00548368
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                 Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89. .90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                         Local Similarity
                                                              Seguence 281 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-1996;
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01-NOV-1995;
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                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TR6; tumour necrosis factor related receptor; human; treatment; stroke; inflammation; arthritis; septicaemia; autoimmune disease; restenosis; transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                          TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKB
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                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 43-44; 62pp; English.
                                                                                                                                                                                                                                                                             infection and for use in assays.
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Goodwin RG;
                                                                      WPI; 1997-118715/11.
N-PSDB; AAT72847.
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This represents a human tumour necrosis factor related apoptosis ligand apoptositide. The human and murine TRAIL polypeptides can induce apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful for producing the recombinant TRAIL polypeptides, which may be useful in studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells feg. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cytokine TNF-related apoptosis ligand polypeptides - u for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 281;
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                      "N-terminal cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 2.9e-266;
live 0; Mismatches 0;
                                                              "transmembrane region"
                                                                                                        /note= "extracellular domain"
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                                   19. .38
/note= "t.
39. .281
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Best Local Similarity 100.
Matches 281; Conservative
  1. .18
/note=
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                                                                                                                                                                                                                                                                                                                                            (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-347322/30.
N-PSDB; AAV29518.
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                                                                                                                                                                                                                                     25-JUN-1996;
                                                                                                                                                                                                                                                                                29-JUN-1995;
                                                                                                                                                US5763223-A.
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                                            Region
                                                                                    Domain
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AAW44354
ID AAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosistinducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, inflammatory can exceed autoimmune disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                DNA encoding tumour necrosis factor receptor TR6 - and corresponding polypeptide, antibody, agonist, antagonist, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 281; DB 2; Length 281; 100.0%; Pred. No. 2.9e-266;
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                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 32-33; 34pp; English
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                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP
                                        97US-0041230P.
97US-00853684.
97EP-00310562
                                                                                  97US-00916625
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N-PSDB; AAV63096.
                                                                                                                                                                     Deen KC, Young PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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23-DEC-1997;
                                        14-MAR-1997;
09-MAY-1997;
                                                                                  22-AUG-1997;
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Query Match Local

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AAW56760;

RESULT 5 AAW56760 Key

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                                                                                                                                                                                                                                                                                                                       The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRALL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay capenders for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus crythematosus, psoriasis, scleroderma, infection-related inflammation) or bone resorption diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDSYWDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEETISTVQEKQQNISPLVRERGPQ 120
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                         Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYXIXSOTYFRFOEEIKENTKNDKOMVOXIXKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                      Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels (
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                                  bone resorption; haematopoietic disease.
                                                                                                                                                                                                Johnson MJ, Simonet WS, Danilenko DM;
                                                                                                                                                                                                                                                                                                   Claim 7; Page 36-37; 54pp; English
                                                                                                                           97WO-US009895
                                                                                                                                                 96US-00660562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     produce recombinant AGP-1
                                                                                                                                                                                                                      WPI; 1998-042194/04
                                                                                                                                                                                                                                 N-PSDB; AAV15295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 281 AA;
                                                                                                                                                                         (AMGE-) AMGEN
                                                                                                                         06-JUN-1997;
                                                         Homo sapiens
                                                                               WO9746686-A2
                                                                                                                                                  07-JUN-1996;
 Human AGP-1
                                                                                                    11-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                     Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; surface receptor; TRAIL protein.
                                                                                                                                                                     Protein associated with neurodegenerative and autoimmune diseases.
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100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
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AAY01517 standard, peptide; 281 AA.
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                                                                                                            (first entry)
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Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens,
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                                                                                                            27-MAY-1999
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This sequence is the human Apo-2 ligand protein, which is recognised by monoclonal antibodies produced by the hybridoma cell lines of the invention. The hybridoma cell lines are deposited under the American Type Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258 and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic assays for Apo-2 ligand, e.g. detecting its expression in specific cells, tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand antibodies which increased apoptosis. They are also useful for the affinity purification of Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated monoclonal antibodies having antigen specificity for Apo-2
ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
-2 ligand serum, and for treating diseases associated with increased
                                                                                                                                                                                                                                                                                                                                     monoclonal antibody; hybridoma cell line; diagnosis;
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                    Human Apo-2 ligand protein sequence.
                                                                                                                              Z
                                                                                                                           AAY81956 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00780496.
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                                                                                                                                                                                                                                                                                                                                                                  therapy; apoptosis; cancer
                                                                                                                                                                                                                                 (first entry)
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Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                  Apo-2 ligand; human;
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N-PSDB; AAA07425.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel human cytokine, designated Apo-2 ligand Apo-2L. The Apo-2L putpeptide can be produced by standard recombinant methodology. Apo-2L is useful for inducing apoptosis in mammalian cancerells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis in mammalian cancer cells.
                                                                                                                                                                                                                                                                                                       Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'connel MT, Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 281; DB 2; I 100.0%; Pred. No. 2.9e-266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                       Human Apo-2 ligand (Apo-2L) polypeptide.
                                                                                                AAY27012 standard; protein; 281 AA
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                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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N-PSDB; AAX86987.
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9936535-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1999;
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15-APR-1998;
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                                                                                                                                                 AAY27012;
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The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO4954; PRO4054; PRO1805; PRO1805; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells.

Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit the present invention can be used to inducing cell death. Methods from the present invention for the present invention to AAC58102 represent PCR primers and hybridisation probes used in camples from the present invention for AAC5812 and AAB24031 to AAB24040 represent human PRO sequences. AAC58103 to AAC5812 and AAB24031 to AAB24040 represent human PRO sequences. Invention
peptides, used to diagnose and inhibit and to identify inhibitors of PRO
                                                                                                                                                                                                                                                                                                          Human; tumour; diagnosis; neoplastic disease; proliferation; cancer; identification; tumourigenesis; anticancer; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy MA, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 281; DB 3; Length 28:
100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0; Indels
                                                 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                           Human PRO1096 protein sequence SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies specific for PRO polypeptides,
the growth of tumors in mammals, and to id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the growth of tumors in mammals, an polypeptide activity or expression.
                                                                                                                                                                      AAB24038 standard; protein; 281 AA
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99US-0162506P.
99WO-US028313.
99WO-US028634.
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                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
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N-PSDB; AAC58120.
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                                                                                                                                                                                                                                                                                                                                                               sapiens.
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30-NOV-1999;
01-DEC-1999;
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                                                                                                                                                                                                                                          25-JAN-2001
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                                                                                                                                                                    240
                                                     DDSYWDPNDEESMNSPCWQVKWQLRQLVRKWILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                        121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                   RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Killing of tumor cells, e.g. solid tumors or carcinoma, comprises administration of synergistic combination of diterpenoid diepoxide and tumor necrosis factor related apoptosis-inducing ligand.
 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                   DDSYWDPNDEBSWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                         FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, TRAIL, tumour necrosis factor, TNF, diterpenoid triepoxide,
TNF related apoptosis-inducing ligand, tumour cell;
TRAIL receptor ligand, solid tumour, carcinoma, mammary carcinoma,
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                                                                                                                                                                                                                                                         SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                       SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 281; DB 3; L
100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human TRAIL polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 23-24; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                           AAB08545 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5-FEB-2000; 2000WO-US003891.
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Length 281;

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Sequence 281 AA;
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08.SEP-1999;
29.OCT-1999;
30.NOV-1999;
01.DEC-1999;
09.DEC-1999;
16.DEC-1999;
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                                                      281;
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Best Local 8
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                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, AGP-1; type II transmembrane protein, cytostatic, antiviral, antiinflammatory; hepatotropic, antiarteriosclerotic, anti-HIV; HIV; human immunodeficiency virus, apoptosis; proliferative disorder; cancer; hepatiis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis.
                                                                                              61 DDSYWDPNDEBSWANSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                   RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                   FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                        DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders.
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                               MANMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
              MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                               FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                        SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                       SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                              AAB28691 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human AGP-1
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                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                   DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                           DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                    181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, PRO; cytostatic; nootropic; neuroprotective; respiratory genera
antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.
                                                 1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                          Gaps
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  Length 281;
                          Indels
                                                                                                                                                                                                                                                                    241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Score 281; DB 3; L
100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           AAB50977 standard; protein; 281 AA
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99WO-US028634.
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99US-0141037P.
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99US-0170262P.
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                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1096 protein.
             Similarity
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17-MAY-2000;
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(GETH ) GENENTECH INC
                                                               WPI; 2001-123012/13.
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                              Sequence 281 AA;
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                               Ashkenazi
O'connell
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Best Local &
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                                                                                 Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
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                                                                                                                                             The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandilar, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
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                                                                                                                                                                                                                                                                                                                                            MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                     Kabakoff RC;
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                                                                                                                                                                                                                                                                                    Length 281;
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                     Henzel W,
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                                                                                                                                                                                                                                                                                   100.0%; Score 281; DB 4; L
100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0;
                    Gurney AL, Hebert C,
Watanabe CK, Wood WI;
                                                                                                                         Claim 31; Fig 54; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB67243 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2000; 2000WO-US017579.
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                                                                                                                                                                                                                                                                                                           281; Conservative
                    Goddard A,
Smith V,
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Apo2 ligand:
                                                   2001-016509/02
                                                                                                                                                                                                                                                                                               Similarity
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                                                              N-PSDB; AAC91579
                                                                                                                                                                                                                                                                Sequence 281 AA;
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                    Baker KP, C
Shelton DL,
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Matches
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                                                                                                                                                                                                                                                                                                                                             The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers
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                                                                                                                                                       Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 281; DB 4; Length 281;
Pred. No. 2.9e-266;
Mismatches 0; Indels (
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   Leung
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/label- N_terminal_cytoplasmic_domain
   RF, Koumenis I,
Simmons L;
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/label= Extracellular_domain
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Hymowitz S, Kelley
Pai R, Shahrokh Z,
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                                                                                                                                                                                                                                                                The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducting ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in timemodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
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                                                                                                                                                                                                New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
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100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                             Claim 2; Col 45-48; 41pp; English
                                                   95US-00496632.
95US-00548368.
96US-00670354.
98US-00048641.
                                99US-00320424
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Matches 281; Conservative
                                                                                                                                            Wiley SR, Goodwin RG;
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                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                2001-595463/67.
                                                                                                                                                                             N-PSDB; AAD18395
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281 AA;
                                26-MAY-1999;
                                                                                     26-MAR-1998;
10-NOV-1998;
                                                                            25-JUN-1996
           04-SEP-2001
                                                      29-JUN-1995
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The invention relates to a human tumour necrosis factor (TNF) related
receptor, TR6. TR6 can be expressed by standard recombinant methodology.
The TR6 polypeptides are useful for treating chronic and acute
inflammation, rheumatoid arthritis, septicemia, autcimmune diseases (e.g.
inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
constitution, stroke, ischaemia, acute respiratory disease
syndrome, asthma, restenosis, brain injury, ADDS, bone diseases, cancer,
atherosclerosis, and Alzheimer's disease. These may also be used to
inhibit production of TNR-alpha and eicosanoids, as research reagents and
materials for discovering treatments and diagnostics to animal and human
diseases. The polypeptides may further be used as immunogens to produce
antibodies immunospecific for the TR6 polypeptides. The polynucleotides
cantibodies immunospecific for the TR6 polypeptides. The polynucleotides
constant also be used as hybridization probes for colbna and genomic DNA, for
isolating full-length cDNAs and genomic clones encoding TR6 and of other
genes having high sequence similarity to TR6 gene, and for chromosome
identification. The present sequence represents a human TL2 polypeptide.
TL2 is also known as TRAIL (TNR-related apoptosis-inducing ligand) and is
a ligand for the TL2 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tumor necrosis factor related receptor TR6 polynucleotides and polypeptides useful for e.g. for treating chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, infection, cancer, bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Tumour necrosis factor; TNF; TNF related receptor; ino; incuration antiinflammatory; immunosuppressive; creebroprotective; vasotropic; antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic; gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
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100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00333593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             L2-JUN-2000; 2000WO-US016134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112223/12.
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                                                                                                                                                                                                                                                                                                           WO200077191-A1.
                                                                                                                                                                                                                                Homo sapiens
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cancer; dendritic cell mobilisation factor; tumour-killing agent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dendritic cell maturation agent; T cell enhancing factor; skin cancer; antigen-appecific T cell; prostate cancer; liver cancer; bone tumour; brain tumour; spinal cord tumour; cervical intraepithelial neoplasia; actinic keratosis; dendritic cell maturation stimulator; cytostatic;
                                                                     RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                         FYY I Y SQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDPI LLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                         FYY1YSQTYFRFQEEIKENTKNDKQMVQY1YKYTSYPDP1LLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating an individual with tumors or cancers, e.g. liver cancer or b tumor, by administering a combination of dendritic cell populations, cell enhancing factors and activated, antigen-specific T cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dendritic cell activator; T cell enhancer; human; TRAIL.
                                                                                                                                                                                                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG31630 standard; protein; 281 AA
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Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism. The method involves administering a combination of two too five agents comprising:

(a) dendritic cell mobilisation factor; (b) dendritic cell maturation agent; (c) dendritic cell activation agent; (d) T cell enhancing factor; or (e) activated, antigen-pecific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria c). T. cruzi, which causes Chaga's disease). The methods are especially useful for treating an individual suffering from immunosuppression by chancing a lymphocyte-mediated immune response. In particular, the method is useful for treating inflammations. C) the pathogen from the connected antifection of the presenting coll leukemia or T call lymphoma. The activated antigen-presenting contains or the cell lymphoma. The activated antigen-presenting contains or the cell lymphoma. The activated antigen-presenting contains or cell lymphoma. The activated antigen-presenting contains contains and contains and contains and contains contains and contains contains contains and contains contains and contains con
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                                                                                                                                                                                                                                                                                                                                                                                                                       Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial; fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV; tuberculostatic; cytostatic; human; TRAIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating an individual suffering from infection, e.g. inflammation, chickenpox or AIDS, by administering a combination of dendritic cell mobilization factor or maturation agent, T cell enhancing factor and
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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ive 0; Mismatches 0;
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a a human TRAIL polypeptide fragment
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                                                                                                                                                                                  ABB08133 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid tripoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, heematological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cells mycosis cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered
            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                          DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                      180
                                                                                                                          TRAIL; TNF; apoptosis; tumour; death domain receptor ligand; diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma; neurological malignancy; haematological lung carcinoma; non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic; malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic; non-MF cutaneous T-cell; lymphoma; mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human.
                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                   Human TNF related apoptosis inducing ligand (TRAIL) protein.
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with other active agents, e.g. anti- metastatic, anti-tumour or anti-angiogenic agents. The potent synersy between the diterpencies and the death domain ligands allows increased killing at equivalent or lower doses, and can sensitise otherwise resistant cells. This sequence represents the human TNF related apoptosis inducing ligand (TRAIL) protein sequence. TRAIL is a death domain receptor used in the used method of the invention in combination with diterpencial triepoxides to kill tumours by induction of apoptosis
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/note= "Apo-2L polypeptide used in method of Claim 18"
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ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                   Similarity
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The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The invention relates to methods of inducing apoptosis in mammalian cells, and especially to the use of Apo-2L receptor agonists and CPT-11 (a chemotherapeutic agent of the topolomerase I inhibitor class) to chemotherapeutic agent of the topolomerase I inhibitor class) to synergistically induce apoptosis in mammalian cells, in particular mammalian cancer cells, and especially colorectal cancer cells (claimed). The cells may be in cell culture or in a mammal, e.g. a mammal suffering from cancer or a condition in which induction of apoptosis in the cells is desirable. A claimed method of treating cancer in a mammal comprises administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is administered about 6-72 hours prior to administration of the Apo-2L receptor agonist. Preferred Apo-2L receptor agonist include Apo-2L ceceptor agonist leads to upregulation of DR4 and DR3 receptors, directing the cells towards an apoptotic pathway rather than cell cycle arrest and possible DNA repair, thus providing enhanced antitumour growth by Apo-2L and CPT-11 in athymic nucle mice injected s.c. with human CUCO205 colon carcinoma cells
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Claim 18; Page 79-80; 84pp; English
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in prepared the product of mutant of an absolute of mutant gorgen and harbouring a mutant spr gene, the product of mutant spr gene cupresses growth phenotypes exhibited by strains harbouring prc mutants.

(1) is useful for producing a polypeptide, by culturing (I) comprising conncier acid encoding the polypeptide, which is heterologous to the strain, usuch that the nucleic acid is expressed, and recovering the chereologous polypeptide from the strain. The heterologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (I) is performed in a fermentor conditions of high- or low-cell density fermentation. The polypeptide is an antibody (humanised or full-length attibody) or Apo2 ligand. The antibody (humanised or full-length attibody) or Apo2 ligand. The antibody (humanised croft). 2C4, anti-vascular endothedial growth factor (VEGF), anti-tissue factor, 2C4, anti-Host antibody (ragment having a light chain (kappa light chain). The antibody creament having a light chain (kappa light chain). The antibody or anti-CD18 apper fusion, anti-tissue factor Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, anti-classe factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor fab'2-leucine zipper fusion with a 6-histidine tag, and anti-classe factor fab'2-leucine zipp
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                                                                                                                                                                                                                                              Novel Escherichia coli strain useful for producing polypeptide, deficient in degP and prc encoding protease, and harboring mutant spr gene, product of gene suppresses growth phenotypes of strains harboring prc mutants.
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100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0;
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  14-DEC-2000; 2000US-0256162P.
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                                                      (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                          Producing a population of activated, Cryptococcus neoformans antigen-
presenting dendritic cells for preventing or treating C. neoformans
infection comprises causing the obtained dendritic cells to present the
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                                 C neoformans antigen expressing dendritic cell related protein #4.
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                                                               Human; fungicide; fungal infection; dendritic cell; antigen;
Cryptococcus neoformans; vaccine; immunostimulant.
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                                                                                                                                                                                                                       14-DEC-2001; 2001WO-US048288
                                                                                                                                                                                                                                                       04-JAN-2001; 2001US-0259653P
22-NOV-2002 (first entry)
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Best Local Similarity
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                                                                                                                                                      WO200266053-A2
                                                                                                                      Homo sapiens
                                                                                                                                                                                     29-AUG-2002
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AAU79593 standard; protein; 281 AA

24-SEP-2002 (first entry)

AAU79593;

RESULT 23
AAU79593
ID AAU79
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AC AAU79
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DT 24-SE

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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNP)-related apoptodis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicallular organisms.

Apoptosis is induced by certain cytokines which include TNF and TRAIL CALL organisms.

Apoptosis is induced by certain cytokines which include TNF and TRAIL CALL organisms.

Apoptosis is induced by certain cytokines which include TNF and TRAIL CALL organisms.

TRAIL is a type II membrane protein and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain correctly by the intracellular signalling death domain. TRAIL, and profession that the showing significant toxic side effects. Thus TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in cheir cellular distribution, expression levels/timing and activity.

Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and the splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytocoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
                                                         Human, cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF: TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B; type I interferon; tumour; anoitumour; gene therapy; cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging;
                  Human TNF-related apoptosis inducing ligand (TRAIL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Extracellular domain"
118. .256
/note= "TNF domain"
                                                                                                                                                                                                                                                                                                                                                                      "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                           "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6-MAY-2001; 2001US-00855544.
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'note=
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(KHOS/) KHOSRAVI R.
(SAVI/) SAVITZKY K.
                                                                                                                                                                                                chromosome 3q26.
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                                                                                                                                                                                                                                           Homo sapiens.
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diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the wild-type human TNF-related apoptosis inducing ligand (TRAIL) protein
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                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                           MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Pred. No. 2.9e-266;
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                                                                                        Mismatches
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100.0%; Pr
tive 0;
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The invention relates to an Apo-3 polypeptide having an extracellular domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide to domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide has been found to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibits similarities to the tumour necrosis factor ceceptor (TNPR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The Apo-3 polypeptide is useful herapeutically to induce apoptosis in mammalian cells. Decreased levels of apoptosis are associated with diseases such as acquired conditions such as cancer, lugus, and herpes virus infection. Increased levels of apoptosis are associated with diseases such as acquired classase, amyotrophic lateral solerosis, multiple solerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial classase, respectivation injury, and toxin-induced liver disease. The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3 may be prepared, in generating antibodies, as standards in assays for Apo-3, in affinity purification techniques, and in competitive-type receptor binding assays. The chimeric containing unknown quantitically to inhibit apoptosis or nuclear factor -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-content numan Apo-2 ligand protein which is also reported to be involved in apoptotic cell death. In the current invention the apoptotic activity of the Apo-2 ligand protein which is also reported to be involved in apoptotic cell death. In the current invention the apoptotic activity of the Apo-2 ligand protein was measured on human lymphoid cells
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Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
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                                                                                                                                                                                    Example 4; Fig 4; 52pp; English
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ovarian cancer; renal cancer; colorectal cancer; melanoma; tetrine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia; gastric cancer; pancreatic cancer; unlval cancer; thyroid cancer; central nervous system cancer; hepatic carcinoma; glioblastoma;
                                                                 Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
                                                                                                                                                 neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; angiogenic disorder; immunologic disorder.
                                   Human neoplasia inhibiting PRO polypeptide PRO1096.
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99US-0141037P.
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 09-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                          US2002192209-A1.
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22-DEC-1998;
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 The invention relates to an isolated Apo-3 polypeptide. The Apo-3 polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antigonistic antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/ inflammatory effects of Apo-3 resulting from NF-kappaB activation. The unclease acts sequences are useful as diagnostics for tissue-specific typing, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOSYMDPNDESSMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                            New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developing and screening of therapeutically useful reagents. The E
sequence represents the amino acid sequence of human Apo-2 ligand
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100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels (
neurodegenerative disease; immunosuppresive; tissue typing.
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                                                                                                                                       28-MAR-2002; 2002US-00112193.
                                                                                                                                                                        96US-0026943P
                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                          2003-438872/41.
                                                                                                                                                                                                                                                                                                          N-PSDB; ACA61696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 281 AA;
                                                                   US2003004313-A1
                                                                                                                                                                                                                                                          Ashkenazi AJ;
                                     Homo sapiens.
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11-SEP-1997;
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Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for treating tumor, preferably cancer, or for treating neuronal, glial, hypothalamic, stromal, inflammatory, angiogenic and immunologic
                                                                                                                                                                                                                                                                       Henzel W, Kabakoff RC;
                                                                                                                                                                                                                                                                      Gurney AL, Hebert C,
Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                    Claim 32; Fig 54; 186pp; English
                                                   2000WO-US014042
                                                                                                                                                             2001WO-US017800
                                                                                                                                                                                                2001US-00918585
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                                                                2000WO-US015264
                                                                      2000WO-US022031
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                                                                                                                                2001US-00866034
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                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                      Goddard A,
, Smith V,
                                                                                                                                                                                                                                                                                           2003-328851/06.
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                           15-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
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                                                                02-JUN-2000;
                                                                               23-AUG-2000;
                                                                                                                                                                                                                                                                            Shelton DL,
                                                                                                                                                                                                                                                                                                                                        disorders.
                                                                                                                                                                                                                                                                       Baker KP,
                                                                                                                                                                                                                             28-AUG-2
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                                                                                                                                                                                                       06-AUG-
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The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its associated signal peptide or PRO polypeptide extracellular domain with or without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour, preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, clader, gastric, pancreatic, vulval, thyroid, central nervous system cancer, hepatic carcinomas, sarcomas, giloblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its agonists. The PRO polypeptide or an antibody binding to it is useful in the preparation of a medicament for treating a condition which is responsive to the PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, erromal, blastocoellc, inflammatory, angiogenic and immunologic disorders. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention

Sequence 281 AA

Query Match

Length 281; DB 6; 100.0%; Score 281;

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                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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   2.9e-266;
                  0; Mismatches
   Pred. No.
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Best Local Similarity
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Human TNF-related apoptosis inducing ligand (TRAIL) protein. ABG72738 standard; protein; 281 AA (first entry) 17-FEB-2003 ABG72738; 

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Human, allergic disease; allergy; TNF; TRAIL; disgnosis; tumour necrosis factor-related apoptosis inducing ligand; atopic skin inflammation.

Homo sapiens.

WO200283946-A1

24-OCT-2002.

01-MAR-2002; 2002WO-JP001914

06-APR-2001; 2001JP-00108631

(GENO-) GENOX RES INC. (NIGE-) JAPAN GEN AGENCY NATION.

Gunji S, Kagaya S, Heishi M, Sugita Y,

Tsujimoto G;

WPI; 2003-093037/08. N-PSDB; ABX13715.

Measurement of the expression level of TNF related apoptosis inducing ligand gene for diagnosis and examination of allergic disease and screening agents for allergic disease treatment.

Disclosure; Page 51-52; 58pp; Japanese.

comprises measuring the expression level of timour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) gene in a specimen from the patient and comparing this level with the level in healthy persons. TRAIL gene expression is decreased in patients. The nucleic acids and polypeptide can be used to screen for agents for the treatment of allergic diseases, possibly using a transgenic rodent as a model animal for the disease, with effectiveness determined by changes in expression levels or protein activity. The method is useful for the diagnosis, examination, prevention and treatment of allergic diseases, including atopic skin inflammation. The sequence presented is the human TRAIL The invention discloses a method for examining allergic diseases, which

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer; hyperproliferative disorder; rheumatoid arthritis; Parkinson's disease; neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease; allergic disorder; acquired immune deficiency syndrome; ocular disorder; myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury; infectious diseases; myelodysplastic syndrome; cardiovascular disorder; cerebrovascular disorder; cerebrovascular disorder; thrombotic microangiopathy; aplastic anaemia; ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis; asthma; AIDS; therapy; TRAIL receptor; TRAIL-R; AIM-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antibody against TNF-related apoptosis inducing ligand, useful for preventing, treating and ameliorating cancers and other hyperproliferative disorders, binds immunospecifically to TRAIL receptor # polypeptide.
                                                                                                                                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                     RVAAHITGTRGRSVTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                      DSYWDFNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                           Length 281;
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                                           100.0%; Score 281; DB 6; I
100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
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07-MAY-2002; 2002US-0377973P.
15-AUG-2002; 2002US-0403376P.
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                                                                   Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                Human TRAIL protein.
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                                                      Local Similarity
                     Sequence 281 AA;
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tumour necrosis factor (TMF) -related apoptosis inducing ligand (TRAIL)

receptors (TRAIL-R). Antibodies of the invention are useful for treating,

receptors (TRAIL-R). Antibodies of the invention are useful for treating,

preventing or ameliotating cancer (e.g. cancers of paroreas, uterine,

breast, colon, lung and gastrointestine and Kaposi's sarcoma) and other

hyperproliferative disorders, neurodegenerative disorders (e.g.

colorimanne disorders, Alaheimer's disease and Huntingfoon's disease),

autoimmune disorders (e.g. lupus, rheumatoid arthritis, multiple

sclerosis, myasthenia gravis, Hashimot's disease and immunodeficiency

syndrome), inflammatory disorders (e.g. asthma, allorgic disorders and

rheumatoid arthritis), infectious diseases (e.g. acquired immune

deficiency syndrome; AlDS, herpes viral infections and other viral

infections), myelodysplastic syndromes (e.g. aplastic anaemia), graft-

cersus-host disease, ischaemic injury, liver injury, toxin-induced liver

disease, septic shock, cachexia, anorexia and proliferative disorders.

Antibodies of the invention are also useful for treating cardiovascular

disorders cerebrovascular disorders, thrombotic microangiopathies,

disorders, cerlar disorders associated with neovascularisation, psoriasis,

and ulcerative colitis and for wound healing. The invention is also used

thopselvery accines. The present sequence is human TRAIL protein also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOSYMDPUDEESMISPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                          The invention relates to antibodies that immunospecifically bind to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TNF Related Apoptosis Inducing Ligand, TRAIL.
Example 2; Page 392-393; 405pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
39. .124
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Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     known as AIM-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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The invention relates to an antibody that specifically binds: (a) the human tumor necrosis factor (TMF) related apoptosis inducing ligand (TMRIL) protein appearing as ABU08558; (b) a soluble human TRAIL polypeptide; (c) a polypeptide comprising amino acids 124-276 of ABU08558, or (d) a fragment of the TRAIL protein. Also included is an antigen-binding fragment of the antibody (a monoclonal antibody), a sasys to detect the presence of TRAIL polypeptides, either in vitro or in vivo, purifying TRAIL by affinity chromatography, blocking binding of TRAIL, to target cells and thus inhibiting a biological activity of TRAIL. The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic transcribed by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic chromotycytopaenic purpura (TTP), adult haemolytic uraemic syndrome (HUS) (even though it can strike children as well) small blood vessel clotting disorders e.g., cardiac problems in paediarric AIDS patients and systemic lupus erythematosus (SLE). The present sequence represents human TRAIL
                 124. .276
/note= "This region is specifically claimed in claim 20"
276. .281
/note= "C-terminal fragment specifically claimed in claim
26"
note= "N-terminal fragment specifically claimed in claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibody which binds to human tumor necrosis factor related apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated apoptosis of a target cell, or blocking binding of TRAIL to a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                    95US-00496632.
95US-00548368.
96US-00670354.
98US-00048641.
                                                                                                                                                                                                                    02-APR-2001; 2001US-00825563
                                                                                                                                                                                                                                                                                                                                                99US-00320424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-340628/32.
N-PSDB; ABX93869.
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                                                                                                                                                                                                                                                                     01-NOV-1995;
25-JUN-1996;
26-MAR-1998;
10-NOV-1998;
26-MAY-1999;
                                                                                                                                               US6521228-B1
                                                                                                                                                                                                                                                        29-JUN-1995;
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The present sequence is the protein sequence of human TRAIL polypeptide.

The invention relates to compositions comprising heterotrimeric complexes of tumour necrosis factor (TNP) ligand family members, and their use in the detection, prevention and treatment of disease. In one embodiment, the heterotrimeric complex comprises full-length or extracellular portions of TRAIL and full-length or extracellular portions of of other TNP ligand family members, preferably RAMIL. The heterotrimeric complexes of the invention are useful for treating an autoimmune disease, cancer or osteoporosis, and particularly for inhibiting cancer cell proliferation, increasing a cells. A claimed method of inducing apoptosis of Teals comprises administering a heterotrimeric complex consisting of FasL and LIGHT, TNP-alpha, the proliferation involves administering a heterotrimeric complex consisting of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New heteromultimeric complex having a first polypeptide member of the tumor necrosis factor (TNF) ligand family, and a second different member of TNF ligand family, useful for treating cancer, osteoporosis or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                Human; TRAIL; tumour necrosis factor; ligand; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
100.0%; Score 281; DB 6; L
100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 364-365; 388pp; English.
                                                                                                                 ABR42313 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                25-JUL-2002; 2002WO-US023782.
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-2001; 2001US-0307838P.
                                                                                                                                                                                                                                                                 immunomodulator; osteopathic
                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-430659/40.
                                                                                                                                                                                                                   Human TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 281 AA;
                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                11-AUG-2003
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                                                                                                                                                 ABR42313;
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The invention relates to an isolated antibody comprising a first amino acid sequence having 95 % identity to a second amino acid sequence of either variable heavy chain or light chain-complementerity determining regions (VHCDR1) /VLCDR2 or VHCDR3/VLCDR3 appearing as ABG71906-ABG71911 being specific for human TRAL1 receptors 1-4 (TNF (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that produces the antibody, an antibody that binds the same epitope on a TR4 polypeptide as the antibodies detailed above, detecting expression of a TR4 polypeptide (or detecting, diagnosing, prognosing or monitoring
                                  180
                                                                                                      240
                                                                                                                    Novel antibody for treating, or preventing disease or disorder, comprises amino acid sequence having identity to other amino acid sequence of either variable heavy/light chain-complementarity determining regions.
DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       light chain variable region TNF-related apoptosis-inducing ligand; antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7; TR10; apoptosis; hyperproliferative disorder; hybridoma cell line; Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease; AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder; Alzheiner's disease; Parkinson's disease; autoimmune disorder; multiple sclerosis; Behcet's disease; lupus erythematosus; inflammatory disease; rheumatoid arthritis; psoriasis; wound healing; cardiovascular disorder; angiogenesis; immune response;
                               FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                       SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; TRAIL receptor; tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA
                                                                                                                                                                                                                                                                                                                                                                                                        Human TRAIL receptor-associated protein.
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                                                                                                                                                                                                                                                                                                 ABG71905 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0248847P.
2000US-0252904P.
2001US-0295018P.
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                                                                                                                                                                                                                                                                                                                                                                     20-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemotherapeutic agent.
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27-NOV-2000;
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61
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                                                                                                                                                                                                                                                               RESULT 31
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cancers, and other hyperproliferative disorders) using the antibodies, a hybridoma cell line selected from the hybridoma cell lines contained in ATCC Deposit No. PTA-2793, PTA-2793, PTA-2729, PTA-2794, PTA-2794, PTA-2799, PTA-
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Best Local Similarity 100.0
Marches 281; Conservative
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Homo sapiens

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The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermatological, immunosuppressive, antiallergic, antiatheumic, antiarthritic, cytostatic, antianaemic, antiallergic, antiasthmatic, neuroprocective, ophthalmological, entiateriosclerotic, antiasthmological, contiateriosclerotic, antipopric, thyromimetic, and haemostatic activity. The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in the sease or disorder such as autoimmune disease, and graft versus host disease (GVHD). The autoimmune disease, and graft versus cerythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody is useful for detecting, diagnosing, prognosing, treating, preventing or ameliorating a disease or disorder associated with abstrant ARRIL or ARRIL receptor expression or aberrant function of ARRIL or ARRIL receptor as autoimmune entitoped autoimmune and inflammatory allowing anthem allowing antennal interopendation or antennal antennal disposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis, uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune system, particularly B cell cancers, immune disorders such as myasthenia gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease, immunodeficiency syndrome, Bruton's disease, infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and proliferative disorders (e.g. leukemia). The present sequence represents the tumour necrosis factor TRAIL
                                                                                                                                                                                                                                                                                                                                            Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 216-217; 225pp; English.
                                                                                                 22-MAY-2002; 2002WO-US016106.
                                                                                                                                                24-MAY-2001; 2001US-0293100P
                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                WPI; 2003-156740/15.
WO200294192-A2
                                                28-NOV-2002.
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Sequence 281 AA; Query Match

DDSYWDPNDESSMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 61 DDSYMDPNDEESMNSPCMQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 240 9 9 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDPI LLMKSARNSCWSKDAEYGLY ö 100.0%; Score 281; DB 6; Length 281; 100.0%; Pred. No. 2.9e-266; ive 0; Mismatches 0; Indels C Best Local Similarity 100. Matches 281; Conservative 61 121 181 g δ g ð g ò ઠે

TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration; hyperproliferative disorder; neurodegenerative disorder; immune disorder; Alzheimer's disease; Parkinson's disease, amyotrophic lateral sclerosis; retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis; rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma; biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder; glomerulonephritis; immune deficiency syndrome; myasthenia gravis; polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock; infectious disease; acquired immunodeficiency syndrome; viral infection; ADS; proliferative disorder; myelodysplastic syndrome; viral infection; schomic injury; myocardial infarction; reperfusion injury; cachexia; anorexia; stroke; cardiovascular disorder; peripheral artery disease; limb ischaemia; arrhythmia; congestive heart failure; neovascularisation; ocular disorder; wound healing; anglogenesis; transplantation; human. AAE36258 standard; protein; 281 AA Human TR4 ligand, TRAIL protein. ; 2001US-0293473P. ; 2001US-0294981P. ; 2001US-0309176P. ; 2001US-0323807P. 07-MAY-2002; 2002WO-US014268. 09-OCT-2001; 2001US-0327364P. 07-NOV-2001; 2001US-0331044P. 14-NOV-2001; 2001US-0331310P. 2001US-0341237P 05-APR-2002; 2002US-0369860P (HUMA-) HUMAN GENOME SCI INC. (first entry) WO200297033-A2. Homo sapiens. 02-AUG-2001; 21-SEP-2001; 25-MAY-2001; 04-JUN-2001; 20-DEC-2001; 26-JUN-2003 05-DEC-2002. AAE36258; RESULT 33 AAE36258 

Vaughan TJ; Rosen CA, Albert VR, Dobson CL, Salcedo T, Ruben SM, WPI; 2003-140454/13.

Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.

Disclosure; Page 300-301; 301pp; English.

The present invention relates to novel antibodies that immunospecifically bind to TRAIL receptor (TR4). Sequences of the invention are useful for bind to TRAIL receptor (TR4). Sequences of the invention are useful for treating preventing or ameliorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in thuman. They are useful for detecting expression of TR4 polypeptide and detecting, diagnosing, prognosing or monitoring cancers and other hyperproliferative disorders. Antibodies of the invention are useful for treating preventing or ameliorating neurodegenerative disorders (e.g. Alzheimer's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease), immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, slopymyositis, immune-related glomenlonephritis, wastehenia gravis, disease, colymyositis, immune-related glomenlonephritis, wastehenia gravis, disorders (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS), herpes viral infections and other viral infections) and proliferative

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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY

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SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281 13-NOV-2002; 2002US-0425737P

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(e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke, myocardial infarction and reperfusion injury), septic shock, cachexia, anorexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral artery diseases such as limb ischaemia, arrhythmia, congestive heart aliure and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and ocular disorders, for wound healing, for promoting anglogenesis and as adjuvants to enhance immune responsiveness to specific antisen e.g. viral antigen. They are also useful in the preparation or recovery from surgery, trauma, radiation therapy and transplantation. The present sequence is human TR4 ligand, TRAIL protein used in the invention
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  disorders. They are also useful for treating myelodysplastic syndromes
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05-AFR-2002; 2002US-0369877P.
04-JUN-2002; 2002US-038628P.
18-JUL-2002; 2002US-036591P.
15-AUG-2002; 2002US-0403370P.
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CV WHCDR1 (heavy chain variable domain complementarity determining region), CVHCDR1 (heavy chain variable domain complementarity determining region), CVHCDR1 (light chain variable domain complementarity determining region), VLCDR2 (light chain variable domain complementarity chain variable domain complementarity determining region), VLCDR2 or variable domain complementarity composed complementarity in the fragment of the apportance of TRAIL (tumour necrosis factor; TNF-related apportable inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer of Kaposi's sarroma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or graft versus host disease, AIDS (acquired immune deficiency syndrome) or graft versus host disease, AIDS (acquired immune deficiency syndrome) or therapy. The present sequence is human TRAIL.
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iive 0; Mismatches 0;
                                                                           Humphreys R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; DNA methylation; cancer; colon cancer.
                                                                                                                                                                                                                                                     Disclosure; Page 297-298; 301pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO25125 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 281; Conservative
                                                                           Salcedo T, Albert VR,
                                    (HUMA-) HUMAN GENOME
                                                                                                               WPI; 2003-569250/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003013099-A1
                                                                                                                                                                                                                 disease, AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 35
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cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comp
                                                                                                     01-OCT-2002; 2002WO-US031210.
                                                                                                                              02-OCT-2001; 2001US-0326622P.
                                                                                                                                                                                Kelley RF, Lindstrom SH;
                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                           WPI; 2003-541400/51.
                                                                                                                                                                                                                      N-PSDB; ADB61470
                                                   WO2003029420-A2
 native; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention.
                            Homo sapiens.
                                                                             10-APR-2003
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                                                                                                                                                                                                                                                                    The invention relates to a combination comprising cDNAs which are expressed in a disorder or process associated with DNA methylation. The combination and cDNAs are useful for diagnosing, staging, treating or monitoring treatment of cancer, e.g. colon cancer and for detecting changes in expression of genes encoding proteins that are associated with DNA methylation. The protein is useful for screening molecules or compounds to identify at least one ligand that binds to the protein and for producing an antibody. The present sequence represents the amino acid sequence of a protein expressed in a disorder or process associated with DNA methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDSYMDPNDESMNSPCWQVKWQLRQLVRKMILRTSETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo-2 ligand; DRS.Apo2L complex; receptor contact region; high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                          process associated with DNA methylation, useful for diagnosing, staging, treating or monitoring treatment of cancer, e.g. colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                             combination comprising cDNAs that are expressed in a disorder or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 281; DB 6; L
100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                 Disclosure; Page 56-57; 66pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Native human Apo-2 ligand protein.
                                                                                                                                Karpf AR;
                         07-MAR-2002; 2002US-00093766.
                                                   19-MAR-2001; 2001US-0277380P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity 100. Matches 281; Conservative
                                                                                                                              Lasek AKW, Jones DA,
                                                                          (LASE/) LASEK A K W.
(JONE/) JONES D A.
(KARP/) KARPF A R.
                                                                                                                                                       WPI; 2003-503249/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                    N-PSDB; ACD42246
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 281 AA;
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence beliably as sequence that differs from the native sequence baying 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at cresidue positions identified from x-ray crystal structure of the cresidue position(s) selected from 20 positions such as $96C, $101C, $111C, $114C, $115C, $114C, $113C, $114C, $113C, $114C, $113C, $101C, $111C, $114C, $113C, $114C, 
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100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
Claim 1; Fig 1; 92pp; English.
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Matches 281; Conservative
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240 240

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61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                           121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                            241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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   181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents the amino acid sequence of a tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEW EMMONINE ALDRA GENE USEful for preparing a composition for treating disease associated with excessive or insufficient bone resorption e.g., osteoporosis, Paget's disease or arterial calcification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; tumour necrosis factor; TNF ligand; endokine alpha; excessive bone resorption disorder; osteoporosis; Paget's disease; arterial calcification.
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                                                               SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                               SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TNF ligand family member #10.
                                                                                                                                                                                                                                                                                         ADC35202 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001; 2001US-0312542P. 30-OCT-2001; 2001US-0330761P.
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor family ligand
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NI J.
ROSEN C A.
NARDELLI B.
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                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                            ADC35202;
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                                                                                                                                                                                                                             RESULT 37
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The present into present the second of the protein present of the present in present in the present in the present of the protein protein the response of cells to treatment with a compound that modulates protein through a carryity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, certaining whether the cells express and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for certaining whether the objections and polypetides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polymucleotides and (2) identifying polymucleotides and sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polymucleotides or polypeptides, and selecting colymucleotides or polypeptides, and selecting colymucleotides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray of polymucleotides that credict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polymucleotides have cytostatic activities, and can be used in gene therapy. The polymucleotides and polypeptides are useful in predicting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a predictor set comprising a plurality of
                                                                                                                                                                                      predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways.
                                                                                                                                            Human src biomarker polypeptide SEQ ID NO:269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; SEQ ID NO 269; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee FY,
ADD14080 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2003; 2003WO-US001981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002US-0350061P.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang F, Fairchild CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-636735/60.
N-PSDB; ADD14676.
                                                                                                                                                                                                                                                                                                                                     WO2003062395-A2.
                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                               01-JAN-2004
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120

MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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                                                                                                                                                                                                                                                                                                                         DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; vulnerary; gene therapy; hypoxia-regulated condition; tumourigenesis, angiogenesis; apoptosis; inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; nitric oxide synthesis; cancer; lschaemic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.
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       and/or
                                                                                                                                                                                                                                                 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                          MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                 FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDPI LLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; disease state; cytostatic; antiinflammatory; ophthalmological;
                                                                                                                                                                                        Gaps
activity of compounds that interact with protein tyrosine kinases an protein tyrosine kinase pathways. These may be used in determining of sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                          Length 281;
                                                                                                                                                     100.0%; Score 281; DB 7; Length 2
100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human disease related protein SegID499.
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05-OCT-2001; 2001GB-00024037.
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                                                                                                                                                                       Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-290046/28.
N-PSDB; ADD19011.
                                                                                                                       Sequence 281 AA;
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                                                                                                                                                         Query Match
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implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antinflammatory, ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention such as tumourigenesis, anglogenesis, appotosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as gytocolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                      This invention relates to novel human genes and gene product which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 281; DB 7; L
Pred. No. 2.9e-266;
; Mismatches 0;
                                                                                         Claim 25; SEQ ID NO 499; 424pp; English
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TNF-gamma-beta protein; inflammat
ulcerative colitis; TRAIL; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Sc
100.0%; Pr
tive 0;
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98US-00005020.
98US-0074047P.
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Matches 281; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 281 AA;
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   injury, retinc
wound healing.
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09-JAN-1998;
09-FEB-1998;
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful cor treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of specifically binds a cDNA. A protein encoded by the cDNA is useful for high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds to identify at least one ligand which specifically binds the protein and encoded by the cDNA with several of molecules or compounds to identify a ligand which specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and compound, therefore identifying a ligand which specifically changes the prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid a sequence of a protein encoded by a cDNA differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                   human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEET1STVQEKQQN1SPLVRERGPQ
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100.0%; Pred. No. 2.9e-266;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 118; 41pp; English
                                                                                                                                                                                                                  30-JUL-2001; 2001US-00919039.
                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-0222113P.
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N-PSDB; ADE76952.
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                                                                                                                                                                                                                                                                                       (KASE/) KASER M R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 281 AA;
                                                                                                                                            US2003108871-A1
                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders.
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                                                                                                                                                                                                                                                                                                                          Kaser MR;
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Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods and compositions for treating or mealiorating a disease or disorder of the gastrointestinal tract. The method involves administering a composition comprising tumour necrosis factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with, or suspected of having the disease or disorder. The antagonist of TNF-gamma-beta is useful for treathing or ameliorating a gastrointestinal tract disease or disorder, specifically an inflammatory bowel disease, eg. Crohn's disease or ulcérative colitis. The present sequence is human invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                               ör
                                                                                                                                                                                                                                                                                                                                                                                            ameliorating a disease or disorders of the gastrointestinal tract, inflammatory bowel disease, Crohn's disease or ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor gamma-beta antagonists for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 281; DB 7; Length 281; Best Local Similarity 100.0%; Pred. No. 2.9e-266; Matches 281; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 140-141; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE76953 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                       Zhang
                99US-00246129.
99US-0131963P.
99US-0132227P.
99US-0134067P.
2000US-0180908P.
2000US-00559290.
                                                                                                                          2000US-0216879P.
                                                                                                                                                                             2001US-0314381P.
2001US-0336695P.
                                                                                                                                                                                                                  23-AUG-2002; 2002US-00226294.
                                                                                                                                            26-MAR-2001; 2001US-0278449P
                                                                                                                                                             2001US-00899059
 98US-00131237
                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                       Rosen CA,
                                                                                                                                                                                                                                                                                                                          WPI; 2003-852773/79.
                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD63912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 281 AA;
                                                                    13-MAY-1999;
08-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                       Νi J,
                                                                                                                        07-JUL-2000;
                                                                                                                                                           06-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                            ameliorating
                                                                                                                                                                               24-AUG-2001;
                                                                                                                                                                                              07-DEC-2001;
                                   30-APR-1999;
03-MAY-1999;
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ADE76953
ID ADE76
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SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducting apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "wild-type Ile may be substituted by Val or Leu at this location in the variant referred to in claim 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "wild-type Asp may be substituted by Asn, Glu or
Gln at this location in the variant referred to in claim
17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "wild-type Gln may be substituted by Arg at this location in the variant referred to in claim 17"
                                                                                                                                                                             Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand variant; cancer; immune system disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "wild-type His may be substituted by Arg, Asp, Asn, Ala, Pro or Thr at this location in the variant referred to in claim 17"
                                                                                                                                                                                                                                                                                                                     /note= "wild-type Tyr may be substituted by Ala,
Xaa (where Xaa is encoded by an amber codon) at t
                                                                                                                                                                                                                                                                                                                                                          ocation in the variant referred to in claim 17"
                                                                                                                                                                                                                                                                                                                                                                                           note= "wild-type Arg may be substituted by Lys ocation in the variant referred to in claim 17"
                                                                                                                                           Human Apo-2 ligand with potential substitutions highlighted #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lindstrom SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO 1; 111pp; English
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                  ADK72311 standard; protein; 281
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                                                                                                        (first entry)
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                                                                     ADK72311;
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                                                                                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                    DDSYWDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEETISTVQEKQQNISPLVRERGPQ 120
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current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 17 may contain one or more of the potential substitutions highlighted in the features table for this record.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic, antiarthritic; neuroprotective, gene therapy, Apo-2 ligand; variant, cancer, immune system disease, arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                  MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGTACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Apo-2 ligand with potential substitutions highlighted #1.
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                                                                                                                       Indels
                                                                                                Length
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                                                                                              Score 281; DB 8; I Pred. No. 2.9e-266;
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                                                                                                                       Mismatches
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100.0%; Pre
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                                                                                                                         281; Conservative
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                                                                                                            Similarity
                                                                      Sequence 281 AA;
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                                                                                                                                                              The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 1 may contain one or more of the potential substitutions highlighted in the features table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDSYMDPNDEESMNSPCWQVXWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                               Jand variant polypeptide, useful for preparing a composition cancer or immune-related disease, e.g., arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                           Lindstrom SH;
                                                                                                                                        Claim 1; SEQ ID NO 1; 111pp; English.
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Misc-difference 189
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Matches 281; Conservative
                                                                               Apo-2 ligand variant treating cancer or in
                           Kelley RF,
(GETH ) GENENTECH INC.
                                                     WPI; 2004-082490/08
                                                                                                              multiple sclerosis.
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S11C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer immune-related disease, e.g., arthritis or multiple sclerosis. The Note: The variant sequence the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 2 may contain one or more of the potential substitutions highlighted in the features table
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                                                       /note= "wild-type Gln may be substituted by Arg, Ser, Thr, Val or Lys at this location in the variant referred to in claim 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or
/note= "wild-type Tyr may be substituted by Ala at this
                                                                                                                                                                                                               /note= "wild-type Asn may be substituted by Gly, Lys, or Arg at this location in the variant referred to in claim 2"
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                                                                                                                                                                                                                                                                                                                                                                                         /note= "wild-type Lys may be substituted by His, Ala, Arg, Gly, Thr or Ser at this location in the variant referred to in claim 2"
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                             ocation in the variant referred to in claim 2"
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Matches 281; Conservative
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                                                                                                                                                                                                               Misc-difference 199
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                                                                                                                                                                                                                                                                                                                                                            Misc-difference 201
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Thr at this location in the variant referred to in claim
10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic, antiarthritic; neuroprotective; gene therapy; Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis;
                                                                                                                                                 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                      FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "wild-type Tyr may be substituted by Ala, Se or Gly at this location in the variant referred to claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "wild-type His may be substituted by Ala, Gly, Gln, Asp, Arg, Pro, Ser, Glu, Asn or Lys at location in the variant referred to in claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Apo-2 ligand with potential substitutions highlighted #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the wild-type human Apo-2 ligand amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 anino acids and having one or more following amino acids substitutions at the residue positions comprising 596C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                        Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis;
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                        241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            Human wild-type Apo-2 ligand, seg id 1.
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                                                                                                                                                                ADK72296 standard; protein; 281
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                                                                                                                                                                                                                                                           (first entry)
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les 281, Conservative
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N-PSDB; ADK72297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 281 AA;
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Matches
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ADK72296
ID ADK72296
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Gln

by Lys or Arg at in claim 10"

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand bolypeptide sequence comprising 282 animo acids and having comprising s96C, 510IC, 811IC, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. The variant sequence that is referred to in claim 10 may contain one or more of the potential substitutions highlighted in the features
New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or
                                                                                                          Claim 10; SEQ ID NO 1; 111pp; English.
                                                      multiple sclerosis.
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Sequence 281 AA;

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                                                                                         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGTACFLKE
                                                                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
                                                                    1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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100.0%; Score 281; DB 8; Length 281; 100.0%; Pred. No. 2.9e-266; cive 0; Mismatches 0; Indels (
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                                    Matches 281; Conservative
                    Local Similarity
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ADJ63976 standard; protein; 281 AA 20-MAY-2004 (first entry) ADJ63976; RESULT 47 ADJ6397( 

Human apoptosis inducing molecule 1, AIM-1.

Human, apoptosis inducing molecule 1, AIM-1, apoptosis, autoimmune disease, graft versus host disease, lymphadenopathy; immunosuppressive, vasotropic, cytostatic, peripheral tolerance; cell activation, cell proliferation; immune regulation, inflammatory response; systemic lupus erythematosus, inflammatory response; systemic lupus erythematosus; immunoproliferative disease; neoplasm; tumour; restenosis.

Homo sapiens

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l. .38
'note≂ "Signal peptide"
                                             /label= Mature_AIM_1
iocation/Qualifiers
                                   .281
            Peptide
                                   Protein
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The invention relates to apoptosis inducing molecule-I protein (AIM-I)

comprising sequence that is 70 % identical to ADJ63976 or its mature form
where the polypeptide binds antibody specific to AIM-I, induces apoptosis

of cell line derived from pathological tissue and induces apoptosis of T

cells. Also included are a composition comprising AIM-I and a carrier,

AIM-I produced by a process involving expressing in a host cell a nucleic

acid that encodes the protein so as to produce the protein (where the

cold that encodes the protein so as to produce the protein (where the

nucleic acid is chosen from a polymucleotide encoding AIM-I, mature AIM
cold that encodes the protein so as to produce the protein (where the

nucleic acid is chosen from a polymucleotide that is complementary to

consisting of 0.5 X SSC (Salline-Sodium Cirrate) and 0.1 % sodium dodecyl

consisting of 0.5 X SSC (Salline-Sodium Cirrate) and 0.1 % sodium dodecyl

sulphate (SDS) to a polymucleotide chosen from polymucleotide encoding

mature/AIM-I, and a polymucleotide chosen from polymucleotide encodes a polypeptide that has the same biological

consisting peripheral toleposit No. 9748, where the

polymucleotide encodes a polypeptide that has the same biological

activity as described above). AIM-I is useful for treating

colding peripheral tolerance, destroying pathologic transformed cell

colding peripheral tolerance, destroying pathologic transformed cell

colding mature/AIM-I is useful for diagnosis and treatment of

inflammatory response, are useful for diagnosis and treatment of

discrets of cells, tissues and organisms. AIM-I is useful as research

colding in elucidating plology of autoimmume disorders including systemic

colding including including including including systemic

colding including including including including systemic

colding including i Novel apoptosis inducing molecule polypeptide that induces apoptosis of cell line derived from pathological tissue and induces apoptosis of T cells, useful for treating lymphadenopathy, autoimmune diseases and graft /note= "Claimed in claim 1" Claim 1; SEQ ID NO 2; 36pp; English. 97US-00816981. .6-SEP-2003; 2003US-00662429 96US-0013405P (HUMA-) HUMAN GENOME SCI INC. WPI; 2004-203230/19. versus host disease N-PSDB; ADJ63975. 14-MAR-1996; 13-MAR-1997; 26-FEB-2004. Ruben SM; 

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMQDKYSKSGIACFLKE Gapa ö 0; Indels 100.0%; Score 281; DB 8; L 100.0%; Pred. No. 2.9e-266; 0; Mismatches Matches 281; Conservative Query Match Best Local Similarity ò

lupus erythematosus, immunoproliferative disease lymphadenopathy and is useful for inhibiting neoplasis such as tumour cell growth. Alm. 1 is also useful to treat diseases which required growth promotion activity e.g., restenosis. Alm.1 is useful for assessing Alm.1 binding capacity of its

binding molecules such as receptor molecules. The present sequence

represents AIM-1.

Seguence 281 AA;

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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 121

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RVAAHITGTRGRSNTLSSPNSKWEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                             181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor necrosis factor related apoptosis inducing ligand polypeptides, useful in studies of apoptosis, in regulating programmed cell death, or for treating leukemia, cancer (e.g. colorectal cancer) or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a new purified tumour necrosis factor related apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid sequence that is at least 90% identical to human TRAIL (ADRISSOS) meanse TRAIL (ADRISSOS). The TRAIL polypeptide induces apoptosis of Jurk cells. Also included are a purified human TRAIL polypeptide encoded by
                                                                            PYX I YSQTYFRFQEEIKENTKNDKQMVQY I YKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                         Human, TRAIL, TNF related apoptosis inducing ligand, apoptosis,
cytostatic, virucide, tumour necrosis factor, Jurkat cell, cancer,
programmed cell death, leukaemia, colorectal cancer, viral infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 4"
                                                                                                                                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Cytoplasmic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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95US-00548368.
95US-00670354.
98US-000408611.
98US-00190046.
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/note= "T
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/note= "E
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                                                                                                                                                                                                                                                                                                                                                                                          Human TRAIL protein.
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26-MAY-1999;
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ADK15498
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                                                                          240
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKG 180
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                                                            181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                            241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                  Human apoptosis inducing molecule-I (AIM-I) protein.
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100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0;
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13-MAR-1997; 97US-00816981.
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Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                            ADL71816;
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Best Local S
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ð 유 ò 셤 97US-00816981.

13-MAR-1997;

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(or a fragment of human TRAIL protein of SEQ ID NO: 2 that induces apoptosis of Jurkat cells, a fusion protein comprising a leucine zipper peptide and a soluble TRAIL polypeptide (Comprising the extracellular domain) and a leucine zipper comprising ADKIS510-ADKIS513, an oligomer comprising at least two soluble TRAIL polypeptides (or at least two fusion proteins defined above), an antibody that specifically binds a TRAIL protein above and a method of inducing death of cancer cells (by an oligomer defined above). The TRAIL polypeptide is useful in studies of apoptosis, in regulating programmed cell death, for treating leukaemia, cancer (e.g. colorectal cancer) or viral infections, or in purifying leukaemic cells or a desired cell surface antigen which can be used in vaccine development. The TRAIL polypeptide may also be used in development.
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   cDNA insert of the recombinant vector deposited in strain ATCC 69849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAMMEVOGGEBIGOTCVLIVIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duery Match 100.0%; Score 281; DB 8; Length 281; Best Local Similarity 100.0%; Pred. No. 2.9e-266; Matches 281; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systemic lupus erythematosus;
immunoproliferative disease lymphadenopathy; IPL;
angioimmunoproliferative lymphadenopathy; AlL; rheumatoid
diabetes; multiple sclerosis; graft versus host disease;
lymphoproliferative disease; lymphadenopathy; neoplasia;
tumour cell growth; restenosis; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of TRAIL. The present sequence represents human TRAIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 281 AA;
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polypeptide and the encoding polymuciocide useful in biological, diagnostic, clinical and therapeutic arts. The invention is useful in treating autoimmune disorders such as systemic lupus erythematosus, immunoproliferative disease lymphadenopathy (IPL), angioimmunoproliferative lymphadenopathy (IPL), rheumatoid arthritis, diabetes and multiple sclerosis, graft versus host disease, lymphaproliferative disease such as lymphadenopathy, in inhibiting neoplasis such as tumour cell growth, in treating restenosis and neoplasis such as tumour cell growth, in treating restenosis and neoplasis such as tumour cell growth, in treating restenosis and sequelting haematopoiesis in endothelial cell development. The invention is useful in chromosome identification and as a diagnostic marker for determining expression of AIM-I polypeptide in tumour cell lines including pancreatic tumour, endometrial tumour and T-cell lymphoma. The invention is also useful in gene therapy. The present sequence is human apoptosis inducing molecule I (AIM-I) protein.
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                                                                                                                                                                     Novel human apoptosis inducing molecule I useful for treating lymphadenopathy, systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                  The present invention relates to apoptosis inducing molecule I (AIM-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 281;
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100.0%; Pred. No. 2.9e-266;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2; 35pp; English
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                                     (HUMA-) HUMAN GENOME SCI INC.
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Matches 281; Conservative
                                                                                                                 WPI; 2004-238497/22
                                                                                                                                    N-PSDB; ADNO7586
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                                                                            Ruben SM:
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DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120

1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

Sequence 281 AA; 

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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NP-kappaB pathway. The invention may be useful for the production of compounds with an antinflammatory, be useful for the production of compounds with an antinflammatory, cytostatic, hepatotropic, virucide, antiarteriosclerotic, antiasthmatic, antiasthmatic, antiasthmatic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder crelated to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's Lymphomas, hematopoletic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic cetodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTV-1, cetodermal dysplasia, immunodeficiency, viral infection, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cabcars related to oberrant acute phase responses, cypudicone, stroke, EAE, autoimmune disorders, disorders related to oberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, crejection, disorders related to aberrant acute phase response, hypercongenital conditions related to organ transplant rejection, disorders related to aberrant signal transduction, crejection, disorders related to aberrant signal transplant crejection, proliferating disorders related to aberrant signal transplant crejection, the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification put
hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-ign syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; influenza; viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; influenza; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carman J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2003; 2003US-0440068P.
12-MAY-2003; 2003US-0469757P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV propagation; human
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N-PSDB; ADR14208.
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100.0%; Score 281; DB 8; Length 2 100.0%; Pred. No. 2.9e-266; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 281, Conservative Query Match

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The present invention describes an antibody or its fragment comprising a VH and VL domain that is at least 80% identical to a VH and a VL domain of any of the 14 sequences given in SEQ ID NO:43 to 56, or a VH and a VL domain of an antibody expressed by any one of the cell lines contained in American Type Culture Collection (ATCC) Deposit numbers PTA-3571, PTA-3570 and PTA-3575, where the antibody specifically binds TR4 (TRAIL receptor). Also described is a pharmaceutical composition for treating or preventing haematological cancer, comprising the antibody or its fragment and a member selected from ibritumomab tiuxetan, imatinib mesylate, bortezomid, and a smac peptide or polypeptide. The antibody has cytostatic activity, and can be used in immunotherapy. The antibody or its fragment can be used for the preparation of a pharmaceutical composition for treating or preventing haematological cancer, e.g. Non-
                                                                                                                                                                                                                                                                                                                                                                antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor; haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma; chronic myelogenous lymphoma; multiple myeloma; chronic lymphocytic leukaemia; scPv; human; TRAIL; TNF-related apoptosis-inducing ligand.
240
                                  FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of an antibody or its fragment the specifically binds to TR4, for t preparation of a pharmaceutical composition for treating or preventing hematological cancer, e.g. Non-Hodgkin's lymphoma, multiple myeloma or
FYY I YSQTYFRFQEEIKENTKNDKQMVQY I YKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                              241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                Human TRAIL amino acid sequence SEQ ID NO:66.
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                                                                                                                                                                                                              ADK82215 standard; protein; 281 AA
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13-NOV-2002;
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Length 281;

Disclosure; SEQ ID NO 36; 169pp; English.

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tumour inhibition, tumour treatment; metastasis; infectious lesion; antigen presenting cell; immunostimulatory cytokine; cytostatic; vulnerary; immunomdulator; melanoma; hepatoma; adenocarcinoma; colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer; laryngeal cancer; badder cancer; head cancer; neck cancer; neral cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer; ovarian cancer; oseophageal cancer; gastric cancer; prostrate cancer; testicular cancer; human.
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              chronic lymphocytic leukaemia. The present sequence represents human tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL), which is used in the exemplification of the present invention.
 multiple myeloma, or
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                                                                                                       100.0%; Score 281; DB 8; Length 281; 100.0%; Pred. No. 2.9e-266; ive 0; Mismatches 0; Indels
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Hodgkin's lymphoma, chronic myelogenous lymphoma,
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                                                                                                                         Best Local Similarity 100.
Matches 281; Conservative
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N-PSDB; ADS87999.
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This invention relates to a novel method of inhibiting or treating a tumour, metastasis or infectious lesion in a subject which comprises administering into or near a site of a tumour or infectious lesion in a subject an antigen presenting cell and an immunostimulatory cytckine or a nucleic acid encoding the cytckine. The invention may be useful for the production of compounds with a cytostatic or vulnerary activity acting as immunomodulators. The method is useful in inhibiting or treating a tumour, metastasis or infectious lesion in a subject, where the size of the tumour, metastasis (where number is also decreased) or infectious lesion is decreased. The tumour is selected from melanoma, hepatoma, adenocarcinoma, colorectal cancer, basal cell cancer, head and neck cancer, renal cell cancer, laryngeal cancer, bladder cancer, head and neck cancer, renal call cancer, pancreatic cancer, pulmonary cancer, cervical cancer, cascer, residual cancer, oseophageal cancer, gastric cancer, prostrate cancer, testicular cancer and breast cancer. The present sequence is that
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2003US-00388838.
2003US-00417375.
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2003US-00663431.
2003US-00737318.
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Matches 281; Conservative
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15-APR-2003; 2
13-JUN-2003; 2
15-SEP-2003; 2
15-DEC-2003; 2
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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-associated proteins. Also included are an expression vector. Comprising the above tecombinant nucleic acid or expression vector, a microarray for detecting comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above.

CC emplement an isolated antibody (or its antigen binding fragment) that an isolated antibody, a pharmaceutical composition comprising the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody of the above polypeptide, a hybridoma that produces the above antibody and a pharmaceutical accipient, a kit for detecting cancer cells (comprising the presence or absence of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polypeptide (or their fragments), methods of screening for an individual, an electronic library comprising the above concer cells in an individual, an electronic library comprising the activity of a CA protein (CAP), methods for detecting cancer activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide in a test cell sample, a method for transminance cells in an individual, an electronic library comprising the activity of a CA protein (CAP) methods seemed and a method for individual and reserved encourage and a method seemed and an electronic library encourage and a method for individual and reserved encourage and a method seemed and a method seemed and a method seeme
                                                                                                                                                                                                                              New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                        Malandro MS;
                                                                                                                                                                                                                                                                                                                                                        claim 18; seqid 36; 310pp; English.
                           (SAGR-) SAGRES DISCOVERY INC
                                                                                     Morris DW,
                                                                                                                                               2004-652914/63.
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                                                                                     Morris DW,
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Sequence 281 AA;

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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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The invention relaters to a novel ibolated nuclear and the propertice of antinflammatory, antiarthritic, antirheumatic, immunosuppressive, costeopathic, antidabetic, dermatological, antipportatic, antidabetic, dermatological, the PRO polypeptide, is agonist, antidaportation may have a use in gene therapy. The PRO polypeptide, is agonist, antidaportation in mamune related disorder such as cystemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, include chronic arthritis, a spondyloarthropathy, systemic solerosis, an idiopathic inflammatory myopathy, Sjogran's syntemic solerosis, antoinmune haemolytic anaemia, autoinmune haemolytic anaemia, autoinmune con finance, immune-mediated renal disease, a demyellnating disease of the central or peripheral nervous system, idiopathic demyellnating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyellnating polyneuropathy, a hepatobiliary disease, infectious or autoinmune chronic active hepatitis, primary cliniammatory bowel disease, granulomatous hepatitis, solerosing cholangitis, inflammatory bowel disease, granulomatous hepatitis, solerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's colisease, asthma, allergic rhinitis, atopic dermatitis, sociasis, an allergic chimitis, atopic dermatitis, poorlasis, or presensitivity, urticaria, an immunologic disease, graft rejection or content of sease, spake, an autoimmune content disease, graft rejection or content of sease, graft rejection or serversents a properson or serversents a properson or serversents and season of the lung.
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                                                                                                                                                                                                   PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
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100.0%; Pred. No. 2.9e-266;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; SEQ ID NO 566; 2940pp; English.
                     ADP23388 standard; protein; 281 AA.
                                                                                                                                                           PRO polypeptide SEQ ID NO:566.
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-2003; 2003WO-US034312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2002; 2002US-0423394P.
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark H, Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-419628/39.
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                                                                                                                                                                                                                                                                                                                                             WO2004041170-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system.
                                                                                                                                                                                                                                                                                                Unidentified.
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                                                                                                             18-NOV-2004
                                                                ADP23388;
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ADP23388
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Wood WI;

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in screening for an endothelial cell disorder or
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                                                                                                                                                                                 Sequence 280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises connecting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at correlates with lymphoedema in where the mutation correlates with lymphoedema in bujects, and with the proviso that the LEC protein is not VEGRA-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antinilammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary
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                                                                                                                                                                                                                                                                                                                                                                                                                           Iymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
inflammatory disease; cancer metastasis; lymphatic system; human.
                                                                                                                                                                                 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                               DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                      RVAAHITGTRGRSVTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
              MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                               DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                    FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                growth; differentiation; blood endothelial cell; BEC;
                                                                                                                                                                                                                       SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                        Human BEC/LEC-related protein sequence SeqID367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 367; 176pp; English
                                                                                                                                                                                                                                                                                                              ADN95444 standard; protein; 280 AA
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                                                                                                                                                                                                                                                                                                                                                                01-JUL-2004 (first entry)
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predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cell prowth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metactasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed protein which is related to the method of the invention.Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.6%; Score 280; DB 7; Le
100.0%; Pred. No. 2.7e-265;
ive 0; Mismatches 0;
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This is the amino acid sequence of human TL2 (also known as TRAIL), which has newly been discovered to be a ligand of human tumour necrosis related receptor TR5 (see AAM7631). This TR5 polypeptide of the invention and TL2 can be used in screening processes for compounds which bind the receptor, or its ligand, and which activate (agonists) or inhibit (antagonists) the receptor or TL2. Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide, administering a nucleic acid that inhibits the expression of the nucleotide sequence encoding the polypeptide and/or administering a polypeptide. The active agents can be used for the ligand, substrate or receptor. The active agents can be used for the creatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), creatment of chronic and acute inflammatory bowel disease, psoriasis), ischaemia, acute respiratory disease syndrome, restenosis, brain injury, atherosclerosis and Alzheimer's disease
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                                        New polynucleotide encoding TRS polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury, AIDS and bone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%; Score 279; DB 2; Le
100.0%; Pred. No. 2.6e-264;
tive 0; Mismatches 0;
                                                                                                                                          Disclosure; Page 17-18; 22pp; English.
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tches 279; Conservative
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polypeptide TL2 Sequence 279 AA;

The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2 assessing the ability of the candidate compound to the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause; chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, inflection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, athersclerosis and Alzabiner's disease. The present sequence represents a TNF-R related

Identifying agonists and antagonists to tumour necrosis factor receptor (TNP-R) related polypeptides (LR1, LR2, LT2 and LT4) - useful for treating stroke, Alzhelmer's disease and AIDS.

(SMIK ) SMITHKLINE BEECHAM CORP

Brigham-Burke MR, Young PR,

WPI; 1999-134308/12

97US-0055513P. 97US-0056980P. 97US-0057550P.

13-AUG-1997; 26-AUG-1997; 29-AUG-1997;

98EP-00304424.

04-JUN-1998;

Disclosure; Page 14-15; 18pp; English

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                                                                 62
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                                                                                                                                                                                                                                                                         181 YIYSQTYPRFQEBIKENTKONDKQMVQYIYKYTSYPDPILLAMKSARNSCWSKDAEYGLYSI
                                                                                              1 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
                                                               MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
                                                                                                                             SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV
                                                                                                                                                                                        AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKGFY
                                                                                                                                                                                                                                                       YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI
                                  Gaps
                                  .
0
 Length 279;
99.3%; Score 279; DB 2; Length 27
100.0%; Pred. No. 2.6e-264;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                     Human Apo-2 ligand (Apo-2L) variant D269A.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY27018 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1999 (first entry)
                              279; Conservative
                 Best Local Similarity
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                                             AAY27018
ID AAY2
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AC AAY2
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ADB61495

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The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immunemediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening disposit techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences Approxice 19 represent specific examples of Apo-2L variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis in mammalian cancer cells.
Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; 
lupus; immune-mediated glomerular nephritis; human; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDSYMDPNDEESMNSPCMQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQBKQQNISPLVRERGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDP I LLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Schwall RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.4%; Score 268; DB 2; Length 281; 100.0%; Pred. No. 1.5e-253; ive 0; Mismatches 0; Indels
                                                                                                                                                        /note= "wild-type Asp is replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                  O'connel MT, Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIYQGGIFELKENDRIFVSVTNEHLIDM 268
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                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page; 86pp; English.
                                                                                                                                       /label= D269A
                                                                                                                                                                                                                                                              99WO-US001039.
                                                                                                                                                                                                                                                                                            98US-00007886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-444397/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 281 AA;
                                                                                                       Key
Misc-difference
                                                   Homo sapiens
                                                                                                                                                                                                                                                            15-JAN-1999;
                                                                                                                                                                                          WO9936535-A1
                                                                                                                                                                                                                                                                                              15-JAN-1998;
                                                                                                                                                                                                                                                                                                              15-APR-1998;
                                                                                                                                                                                                                            22-JUL-1999
                                                                     Synthetic
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence to polypeptide having a sequence that differs from the native sequence complex and all and a polypeptide having substitutions at the polypeptide having the substitutions at the polypeptide having the substitutions and at the polypeptide having the substitutions and at the polypeptide having the substitutions and at the cresidue position is, outside of the receptor contact region of the respitue position is, outside of the receptor contact region of the respitue position is, outside of the receptor contact region of the respitue position is, outside of the receptor contact region of the CRS. Apo2L compositions have the following activities of the DRS. Apo2L compositions have the following activities cypeptide, and further compositions have the following activities cypeptide, and and ruther composition or an Apo-2 ligand variant polypeptide, and and ruther composition or an Apo-2 ligand variant polypeptide, contacting apoptosis in mammalian cells, by exposing mammalian cells are expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, and anthrities or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or the mammal and effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or the mammal and effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or the mammal and the sequence represents the human Apo-2 ligand variant polypeptide, Apo-2 ligand variant polypeptide, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                Apo-2 ligand; DRS.Apo2L complex; receptor contact region;
high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
trimer; apoptosis; DR4 receptor; DR5 receptor; colorectal cancer;
lung; breast; immune-related disease; arthritis; multiple sclerosis;
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                                                                                                                                     Juman Apo-2 ligand protein mutant H264C.
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
ADB61495 standard; protein; 281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2001; 2001US-0326622P
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kelley RF, Lindstrom SH;
                                                                                                                                                                                                                                                                              human; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 264
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                                                                                          04-DEC-2003
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                                                                                                                                                                                                                                                                                                                         Synthetic
                                             ADB61495;
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181 FYXIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
                                                                                                                    DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                     DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                              comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo-2 ligand; DR5.Apo2L complex; receptor contact region; high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the naitive sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at
                                                         1 MAMMEVQGGPSLGQTCVLLVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                           MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, commanno acid substitutions in the native sequence of the Apo-2 ligand.
                              ..
Length 281;
                             0; Indels
93.6%; Score 263; DB 7; Le
100.0%; Pred. No. 1.2e-248;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Apo-2 ligand protein mutant E263C.
                                                                                                                                                                                                                                                                                                 SIYOGGIFELKENDRIFVSVTNE 263
                                                                                                                                                                                                                                                                                                                  SIYQGGIFELKENDRIFVSVTNE 263
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Misc-difference 263
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                             Matches 263; Conservative
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               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo-2 ligand;
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Query Match
Best Local 8
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cc residue positions identified from x-ray crystal structure of the DBS.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as 596C, 5101C, 5111C, V114C, R115C, E116C, M134C, M140C, E144C, M152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the CRS.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, and and neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for the Apo-2 ligand sariant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand trimer is useful for the Apo-2 ligand sariant by administering to the mammal an effective amount of the Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand composition or Apo-2 ligand cummant E263C trimer. This secuence represents the human Apo-2 ligand mitant E263C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trimer. This sequence represents the human Apo-2 ligand mutant E263C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDSYNDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEET1STVQEKQQN1SPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNBLKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and from the sequence in Fig 1 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 262; DB 7; Le
100.0%; Pred. No. 1.1e-247;
iive 0; Mismatches 0;
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Les 262; Conservative
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

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01-OCT-2002; 2002WO-US031210.
                               02-OCT-2001; 2001US-0326622P.
                                                                        Claim 1; Page; 92pp; English
                                             Kelley RF, Lindstrom SH;
                                      (GETH ) GENENTECH INC.
                                                   WPI; 2003-541400/51
Misc-difference 255
                                                                                                                                                                                      Sequence 281 AA;
         WO2003029420-A2
                 10-APR-2003
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 DOSYWDPNDEESMNSPCWQVKWQLRQLVRKKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 FYYIYSQTYFRFQEEIKENTKNDKQMVQXIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE Gaps ö Score 254; DB 7; Length 281; Pred. No. 7.6e-240; 0; Indels 100.0%; Pred. .... 90.48; Matches 254; Conservative Query Match Best Local Similarity 61 121 121 61 181 ð 요 ઠે g 8 ద ò

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence blaving 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at cesidue positions identified from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions made at cesidue position(s) selected from 20 positions such as 596C, $101C, $111C, $114C, $115C, $116C, $114C, $115C, $153C, $101C, $111C, $114C, $115C, $116C, $111C, $114C, $115C, $115C, $116C, $11CC, $116C, $11CC, $116C, $11CC, $116C, $11CC, $116C, $11CC, $11CC, $116C, $11CC, $116C, $11CC, $116C, $11CC, $116C, $11CC, $11CC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo-2 ligand, DR5.Apo2L complex; receptor contact region; high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Native residue of Glu is substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Apo-2 ligand protein mutant E249C.
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                                                                                                241 SIYOGGIFELKEND 254
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                                 241 SIYQGGIFELKEND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence polypeptide having a sequence that differs from the native sequence comparing a sequence that differs from the native sequence comparing a sequence comparing the substitutions at the polypeptide having the substitutions at the polypeptide having the substitutions at comparing the substitutions at the polypeptide having the substitutions at the comparing the substitutions at the comparing the substitutions at the polypeptide having the substitution of the composition is, outside of the receptor contact region of the constitution is, outside of the receptor contact region of the constitution of the DRS. Apo2L complex. The Apo-2 ligand variant polypeptide, and further compositions have the following activities of the properties of the proposition or an Apo-2 ligand variant polypeptide, and apo-2 ligand composition or an Apo-2 ligand variant polypeptide, contacting apoptosis in mammalian cells. Wherever, the mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, colorectal cancer cells. The Apo-2 ligand variant polypeptide, colorectal cancer (such as arthritis or multiple sclerosis) in a commune related disease (such as arthritis or multiple sclerosis) in a commune. This sequence represents the human Apo-2 ligand cumposition or the mammal an effective amount of the Apo-2 ligand composition, worked the mammal an effective amount of the Apo-2 ligand composition or the mammal an effective amount of the Apo-2 ligand composition or the mammal and colorectal cancer (such as arthritis or multiple sclerosis) in a community of the human Apo-2 ligand composition or the human Apo-2 ligand composition or the human Apo-2 ligand composition or the human Apo-2 liga
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/note= "Native residue of Arg is substituted by Cys"
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Claim 1; Page 13; 21pp; French.
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Escherichia coli.
                                                                                                                                       Sequence 281 AA;
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13-JUN-2001
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mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant E249C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.
                                                                                                                                                                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                    RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                             MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                   DDSYWDPNDEESWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurodegenerative disease; autoimmune disease; inflammatory disease;
lupus erythematosus; rhuematoid arthritis; SEP; apoptotic;
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein associated with neurodegenerative and autoimmune diseases.
                                                                                                          ;
0
                                                                                       88.3%; Score 248; DB 7; Length 281; 100.0%; Pred. No. 5.6e-234; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Gly or Cys"
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                                                                                                                                                                                                                                                                                                                                                        standard; peptide; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface receptor; TRAIL protein
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                                                                                                Best Local Similarity 100.
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                      SIYQGGIF 248
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                                                                    Sequence 281 AA;
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The specification describes the use a polypeptide corresponding to at least the primary sequence of part of the present sequence to produce a diagnostic, probhylatic or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, lupus erythematosus, rhuematoid arthritis, and SEP. The polypeptides are apoptoric in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific
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    266
    note= "Mature human TNP-alpha-related apoptosis-inducing"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour necrosis factor; TNF, anti-angiogenic factor; cytotoxic polypeptide; tumour inhibitory enzyme; therapy; carcinoma; melanoma; lymphoma; Barcoma; metastasis; cytostatic; fusion protein; TNF-alpha-related apoptosis-inducing ligand; TRAIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.8%; Score 244; DB 2; Le
100.0%; Pred. No. 4.6e-230;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OmpA signal peptide-human TRAIL fusion protein.
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/label- OmpA_signal_peptide
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(first entry)
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108 244; Conservative
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Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

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The present invention relates to the preparation and use of attenuated tumour-targetted bacteria, such as, e.g., Salmonella, as a vector for the tumour-targetted bacteria, such as, e.g., Salmonella, as a vector for the delivery of one or more primary effectors molecules and secondary effector molecules to the site of a solid tumour. The primary effector molecules of the invention include members of the tumour necrosis factor (TNF), anti-anglogenic factors, cytotoxic polypeptides and tumour inhibitory enzymes. They induce a local immune response at the site of the tumour that results in the inhibition of growth of a tumour or tumour cells. The primary effector molecules are used for the treatment of solid tumours cuch as carcinomas, melanomas, lymphomas, sarcomas or metastases derived from these tumours. The present sequence is OmpA signal peptide to the amino of TRAIL) fusion protein. The fusion of OmpA signal peptide to the aminot terminus of TRAIL effector molecule enhances the periplasmic localisation and subsequent processing of the effector molecule. (Updated on 11-SEP-2003 to standardise OS
                                                                                                                                                                                                                                                                              Attenuated tumor-targeted bacteria comprising nucleic acids encoding primary and secondary effector molecules, useful for the treatment of e.g. carcinomas, melanomas, lymphomas and sarcomas.
                                                                                                                                                                           Belcourt M;
                                                                                                                                                                           Lin SL,
                                                                                                                                                                           Clairmont CA,
                                                                                                                                                                                                                                                                                                                                                                      Example 7; Fig 6; 185pp; English.
                                        99US-0157500P.
99US-0157581P.
99US-0157637P.
24-AUG-2000; 2000WO-US023242
                                                                                                                                                                         King IC,
                                                                                                                              (VION-) VION PHARM INC
                                                                                                                                                                                                                      2001-245063/25.
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                                                                                                                                                                         Bermudes DG,
                                          04-OCT-1999;
04-OCT-1999;
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Sequence 266 AA;

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                                                                                                      100 ISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS
                                                                                                                                                               GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQWVQXIYKYTSYPDF
                                                       40 NELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEET
                                                                      NELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEET
                                                                                                                   85 ISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS
                                                                                                                                                    GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP
                                                                                                                                                                                                   ILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL
                               Gaps
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       Length 266;
                              0; Indels
        Score 242; DB 4;
Pred. No. 4e-228;
86.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                Matches 242; Conservative
                    Local Similarity
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Human Apo-2 ligand protein mutant D234C.
                      ADB61491 standard; protein; 281 AA
                                                                  04-DEC-2003 (first entry)
                                             ADB61491;
RESULT 66
          ADB61491
ID ADB
XX
AC ADB
XX
DT 04-I
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Gaps

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0; Indels

82.9%; Score 233; DB 7; Le 100.0%; Pred. No. 2.7e-219; 100.0%; Pred. ...

Conservative

Matches 233;

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Query Match Best Local S

Similarity

9 9

1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence polypeptide having a sequence that differs from the native sequence compared as a sequence that differs from the native sequence compared as a sequence of the polypeptide is selected from x-ray crystal structure of the DRS.Apo2L complex. The polypeptide having the substitutions and at the polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, S101C, R170K, R170S, K179C, E249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DRS.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, and neuroprotective. The Apo-2 ligand variant polypeptide and further composition or an Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells captured the apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide, therapeutically effective amount of the Apo-2 ligand variant polypeptide. Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or coloner and apo-2 ligand trimer. The mammalian cells for the colon or coloner and apple the coloner coloner coloner and apple the coloner coloner coloner and apple the coloner coloner coloner and apple the coloner coloner coloner coloner and the coloner coloner coloner coloner and coloner c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2
                     high solvent accessibility; cytostatic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        information provided in claim 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant D234C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim
                                                                                                                                                                                                                                                                                                                              /note= "Native residue of Asp is substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and from the sequence in Fig 1 of the specification.
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002; 2002WO-US031210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2001; 2001US-0326622P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 92pp; English.
                                                                                                                  human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kelley RF, Lindstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-541400/51.
                                                                                                                                                                                                                                                                                            Misc-difference 234
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                                                                                                                                                                                                                                                                                                                                                                                     WO2003029420-A2
                                                                                                                                                                                                        Homo sapiens
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180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine, Apo-2 ligand, Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.
                                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                           FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLLMKSARNSCWSK 233
                                                                                                                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYTSYPDFILLMKSARNSCWSK 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= D218A
/note= "wild-type Asp is replaced with Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Apo-2 ligand (Apo-2L) variant D218A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY27017 standard; protein; 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US001039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in mammalian cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Misc-difference
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AAY2701 6
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77.2%; Score 217; DB 2; Length 281; 100.0%; Pred. No. 1.2e-203; ive 0; Mismatches 0; Indels

Query Match 77.2 Best Local Similarity 100. Matches 217; Conservative

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The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-21). The Apo-21 polypeptide can be produced by standard recombinant methodology. Apo-21 is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-21 can be used to induce apoptosis for pathological conditions characterized by decreased induce apoptosis, eg. autoimmune disorders like lupus and immune mediated glomerular nephritis and cancer. Apo-21 and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic
                                                                                         120
                                                             DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                        RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                            RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; autoimmune disorder;
                                                                             DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwall
                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmur
lupus; immune-mediated glomerular nephritis; human; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                 Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
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                                                                                                                                                                                         FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYP 217
                                                                                                                                                                                                      FYYIYSQTYFRFQEEIKENTKONDKQMVQYIYKYTSYP 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= D218A
/note= "wild-type Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                    AAY27019 standard; protein; 281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= D203A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= D269A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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Homo sapiens
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techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-2L variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A
                                                                                                                                                        120
                                                                                                                                                                   DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                              180
                                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel human cytokine, designated Apo-2 ligand (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
                                                                                                                                                                                                                                                                                                                                                                                Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.
                                                                                                                               MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                        DDSYWDPNDEESMNSPCWOVKWQLRQLVRKMILRTSEETISTVQBKQQNISPLVRERGPQ
                                                                                                                                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                   1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                Gaps
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                                                                             Length 281;
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                                                                                              Indels
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                                                                             Score 202; DB 2; Le
Pred. No. 5.8e-189;
                                                                     71.9%; Sco...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Human Apo-2 ligand (Apo-2L) variant D203A.
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                                                                                                                                                                                                                                    FYYIYSQTYFRFQEEIKENTKN 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                       standard; protein; 281
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                                                                                      Best Local Similarity 100.
Matches 202; Conservative
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                                                                                     Similarity
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Misc-difference
                                                          Sequence 281 AA;
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15-APR-1998;
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cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like luques and immunementated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences AX27016-19 represent specific examples of Apo-2L variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                          Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour related apoptosis inducing ligand (Trail)
                                                                                                                                                                                                                                                                                                                                                                                             71.9%; Score 202; DB 2; L 100.0%; Pred. No. 5.8e-189; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 10 (disclosure); 17pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA
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Best Local Similarity 100.
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N-PSDB; ABX14391.
                                                                                                                                                                                                                                                                                                                                        Sequence 281 AA;
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The present invention relates to the isolation of cDNA encoding human tumour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Traillo9 and Trail 114, and respectively create Traill09 cDNA and Traill14 cDNA prokaryotic expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Traill09, and Traill14 proteins, and may be useful in a new preparation for killing tumour cells. The present sequence represents the full length human Trail
                                                                                                                                                                                                                                                                                                                                                                              DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type I interferon, tumour; antitumour; gene therapy, cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging; chromosome 3q26; rpl-6-6.
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                                                                                                                                                                                                                                                                                                                                1 MAMMEVQGGFSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                           1 MAMMEVQGGPSLGQTCVLIVIPTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                        70.8%; Score 199; DB 5; Length 281; 100.0%; Pred. No. 5e-186; ive 0; Mismatches 0; Indels
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/note=
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                        Sequence 281 AA;
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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

Collular differentiation and development of multicellular organisms.

Collular differentiation and development of multicellular organisms.

Collo referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DCRI and DCR2, lacking the intracellular signalling death domain. TRAIL included by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic and boxy. Thus, TRAIL has the potential to be a very useful cantitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity.

Collectrining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polyuncleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cyctotoxic effect in cancer cells and for treatment of diseases which can the antibodies may also have a therappeutic the amino acid sequences, are useful for causing and expression of sequences. The amino acid sequences, diseases that may be treated include cancer, neurodegenerative cutility in blocking or decreasing the ameliorated, res
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                                                                                                                                                                                                New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.
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100.0%; Pred. No. 3e-180;
ive 0; Mismatches 0
                                                                                                  Savitzky K;
                                                                                                                                                                                                                                                                                                     Claim 4; Fig 8; 29pp; English
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                                                                                                  Khosravi R,
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Best Local Similarity
(YELI/) YELIN R.
(KHOS/) KHOSRAVI
(SAVI/) SAVITZKY
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RESULT 72 ADK72306

Wed Jun 22

ADK72306 standard; protein; 281 AA.

ADK72306

us-10-662-429-2.oligo.rag

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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand bolypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents a human Apo-2 ligand mutant. Note: This sequence is not found in the specification, but may be created using the wild-type Apo-2 ligand sequence given in ADK72296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis.
                                                                                                                                      Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis;
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                                                                                                                                                                                                                                                                                               note= "wild-type Tyr replaced by Ala"
                                                                                                                                                                                                                                                                                                                               "wild-type Arg replaced by Lys"
                                                                                                                                                                                                                                                                                                                                                                'note= "wild-type Gln replaced by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                /note= "wild-type His replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lindstrom SH;
                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                    Human Apo-2 ligand variant #2
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                                                                    06-MAY-2004 (first entry)
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Best Local Similarity 100.
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 264
                                                                                                                                                                                                                                                                                                             Misc-difference 191
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                                                                                                                                                                        human; mutein.
                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                              Synthetic
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents a human Apo-2 ligand mutant. Note: This sequence is not found in the specification, but may be created using the wild-type Apo-2 ligand sequence given in ADK72296.
             New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or
                                                                                                                                                                                                                                                                                                 Cytostatic, antiarthritic; neuroprotective; gene therapy; Apo-2 ligand; variant; cancer; immune system disease; arthritis; multiple sclerosis;
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "wild-type Arg
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                                                                                                                                                                        ADK72313 standard; protein; 281 AA.
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                                                                                                                                                                                                                                                                    Human Apo-2 ligand variant #7.
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                                                                                                                                                                                                                                      (first entry)
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                                                              FYYIYSQT 188
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                                                                                      181 FYYIYSQT
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                                                                                                                                                                                                                                                                                                                                human; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for preparing a composition disease, e.g., arthritis or
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                                                                                                                                                                                                 61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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              66.9%; Score 188; DB 8; Le
100.0%; Pred. No. 2.9e-175;
ive 0; Mismatches 0;
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                Query Match
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variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents a human Apo-2 ligand mutant. Note: This sequence is not found in the specification, but may be created using the wild-type Apo-2 ligand sequence given in ADK72296.
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100.0%; Pred. No. 2.9e-175;
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                   Sequence 281 AA;
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand bollypeptide sequence comprising 382 amino acids and having one or more following amino acids substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents a human Apo-2 ligand mutant. Note: This sequence is not found in the specification, but may be created using the wild-type Apo-2 ligand sequence given in ADK72296.
                                                                                                 New Apo-2 ligand variant polypeptide, useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or
     Lindstrom SH;
                                                                                                                                                                                                        Claim 9; Page; 111pp; English
Hymowitz S, Kelley RF,
                                                    WPI; 2004-082490/08
                                                                                                                                                      multiple sclerosis.
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Sequence 281 AA;

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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 61 DDSYWDPNDEESWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180 9 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60 1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE 0; Gaps Query Match 66.9%; Score 188; DB 8; Length 281; Best Local Similarity 100.0%; Pred. No. 2.9e-175; Matches 188; Conservative 0; Mismatches 0; Indels FYYIYSQT 188 FYYIYSQT 188 181 181 g g g a ð ò ò ò

Search completed: June 22, 2005, 06:48:54 Job time : 172 secs

Perfect score:

Sequence:

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OM protein

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Scoring table:

98

Minimum D Maximum D

Database

Word size

Searched:

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Sequence 66, Applisequence 2, Applisequence 1, Applisequence 2, Appliseque
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Sequence 12, Appl
Sequence 20, Appl
Sequence 33427, A
Sequence 11, Appl
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4 US-10-218-547-20
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Sequence 11, Appli
                                                                                  ; Search time 161 Seconds
(without alignments)
670.176 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                      1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                               1714042
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-971-317A-8
US-09-813-329-17
US-09-133-663-8
US-09-934-465-1
US-09-934-93-118
US-10-011-125-4
US-10-001-054-54
US-10-0174-654-11
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                             protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Score

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281 281 281 281 281 281 281 281 281

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                                                                                                                                                                                                                                                                                                                 240
                                                                                             61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                                                                                                                                                      181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                      61 DDSYWDPNDEBESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                        181 FYYIYSQTYFRFQEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDABYGLY
         1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                          241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                             241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08971317A

Publication No. US20010010925A1

GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES:
ORRESSONDENCE ADDRESS:
STREET: 100 Abbott Park Road
CITT: Abbott Park Road

STATE: 110 Abbott Park Road

STATE: 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 281; DB 8; I 100.0%; Pred. No. 6.4e-272;
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COUNTRY: USA
ZIP: GOO64-3200
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FRAEESQ for Windows
SOFTWARE: 17-NOV-1997
CLASSIFICATION DATA:
FILING DATE: 17-NOV-1997
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 17-NOV-1997
FLING DATE: 17-NOV-1997
APPLICATION NUMBER:
FILING DATE:
FI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: No. US20010010925Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (847) 938-2623
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 281; Conservative
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Sequence 11, p
Sequence 32, p
Sequence 15, p
Sequence 15, p
Sequence 6, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
APPLICANT: VOUNG, PETER R.
; TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET:
P.O. BOX 980
CITY: VALLEY FORGE
US-10-272-411-24

US-10-272-328A-24

7 US-10-625-073-14

US-09-779-050A-17

US-09-779-050A-17

US-10-652-074-6

US-10-652-244-6

US-10-652-244-6

US-10-17-91.0-6

US-10-1890-368-13

US-10-1890-388-13

US-10-889-948-13

US-10-889-948-13
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ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE CONTROL CALLON DATA:
APPLICATION NUMBER: US/08/916,625B
FILING DATE: 22-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/853,684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041,230
APPLICATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
TELEY: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 281 amino acids
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100.0%; Pred. No. 6.4e-272;
iive 0; Mismatches 0;
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100.0%; Pred. No. 6.4e-272;
ive 0; Mismatches 0;
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/065,916
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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APPLICANT: ASHACHAZI, AVI J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REPERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DAFE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
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Best Local Similarity 100.
Matches 281; Conservative
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CORGANISM: Homo sapiens
US-09-934-465-1
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ORGANISM: Homo sapiens
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Matches 281
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TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT APPLICATION NUMBER: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
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Patent No. US200055624A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: THF-DELTA LIGAND AND USES THEREOF
FILE REFERNE: 6255.US. 02
CURRENT APPLICATION NUMBER: US/09/193,663
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Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0;
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Patent No. US20020012968A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 17
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US-09-193-663-8
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FILE REPREMENCE: P3024R1PCT;
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT PILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/079920
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-30
PRIOR PLING DATE: 1998-04-24
PRIOR PLING DATE: 1998-04-24
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-12
PRIOR PLING DATE: 1998-05-12
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-08-17
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                                               100.0%; Score 281; DB 13;
100.0%; Pred. No. 6.4e-272;
iive 0; Mismatches 0;
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Publication No. US20020192209A1
GENERAL INFORMATION:
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Wood, William
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Shelton,David
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                                                                        Similarity
     US-10-011-125-4
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Publication No. US20030108871A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENE EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION UNDHER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
SOFTWARE: PERL PROGram
SEQ ID NOS: 401
SEQ ID NO 118
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118
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                                                                           SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 281; DB 10;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0;
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; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APALICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                          US-09-919-039-118
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US-10-011-125-4
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APPLICATION NUMBER: 60/141037
FILING DATE: 1999-06-23
APPLICATION NUMBER: 60/144758
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FILLING DATE: 2000-03-03
APPLICATION NUMBER: 60/209832
FILLING DATE: 2000-06-05
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115558
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APPLICATION NUMBER: 09/403297
FILING DATE: 1999-10-18
APPLICATION NUMBER: 09/423741
FILING DATE: 1999-11-10
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FILING DATE: 2001-06-14
APPLICATION NUMBER: 09/918585
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FILING DATE: 1998-12-22
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APPLICATION NUMBER: 60/116533
FILING DATE: 1999-01-20
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APPLICATION NUMBER: 09/218517
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FILING DATE: 1999-08-25
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APPLICATION NUMBER: 09/866034
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APPLICATION NUMBER: 09/9
FILING DATE: 2001-08-13
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PRICES PULING DATE: 2001-00-29

PRICES APPLICATION NUMBER: 07/1859/18614

PRICES APPLICATION NUMBER: 07/1859/00106

PRICES APPLICATION NUMBER: 07/1859/00106

PRICES PLING DATE: 1999-01-06

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Legal Services
STREET: 301 Henrietta Street
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MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version, #1.25
CURRENT APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
ATTORNEY/AGENT INFORMATION:
NAME: Kerber LONIONER: 41,113
REFERENCE/DOCKET NUMBER: 41,113
TELEFRATION INFORMATION:
TELEFRAM: 616/833-0974
TELEFRAM: 616/833-0974
                                                                                            241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TNF-Related Death Ligand NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                              APPLICANT: Bienkowski, Michael J
Mills, Cynthia J
Jones, David A
                                                                                                                                                                                                                              ; Sequence 11, Application US/10174654; Publication No. US20030044937A1; GENERAL INFORMATION:
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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Matches 281; Conservative
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STATE: MI
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APPLICANT: LASEK, Amy W.
APPLICANT: Jones, David A.
APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
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                                                                                                                                                                                      Length 281;
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OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
                                                                                                                                                                                                                                 Indels
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100.0%; Pred. No. 6.4e-272;
iive 0; Mismatches 0;
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US-10-093-766-54
Sequence 54, Application US/10093766
Publication No. US20030013099A1
GENERAL INFORMATION
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 54
LENGTH: 281
                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                               ; ORGANISM: Homo Sapien
US-10-001-054-54
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Best Local Similarity
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LENGTH: 281
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61 DDSYWDPNDEESRMSPCWQVKWQLRQLVRKMILRISEETISTVQEKQQNISPLVRERGPQ 120
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Publication No. US20030180296A1;
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL;
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF585
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                                             Indels
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100.0%; Score 281; DB 14;
100.0%; Pred. No. 6.4e-272;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2002-04-04

PRIOR PILING DATE: 2002-06-04

PRIOR PILING DATE: 2002-06-18

PRIOR PILING DATE: 2002-06-18

PRIOR PILING DATE: 2002-06-18

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-08-15

PRIOR PILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 72

LENGTH: 281
Query Match
Best Local Similarity 100.
Matches 281; Conservative
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Best Local Similarity 100.
Matches 281; Conservative
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ORGANISM: Homo sapiens
US-10-322-673-72
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; Publication No. US20030100074A1
; GENERAL INFORMATION:
; TAPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
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                                                                                                                                                                                                             TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PFS54
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT PILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
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                         241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR PILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 20
LENGTH: 281
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Publication No. US20030059862A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches ~281; Conservative
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; ORGANISM: Homo sapiens
US-10-151-882-41
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US-10-218-547-20
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US-10-218-547-20
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APPLICANT: Ni, Jan
APPLICANT: Ni, Jan
APPLICANT: Rosen, Craig A
APPLICANT: Wei, Ping
ITILE OF INVENTION: Relating To Human Tumor Necrosis Pactor-Gamma Beta
ITILE OF INVENTION: Relating To Human Tumor Necrosis Pactor-Gamma Beta
ITILE OF INVENTION: Relating To Human Tumor Necrosis Pactor-Gamma Beta
CURRENT APPLICATION NUMBER: US/10/310,793
CURRENT APPLICATION NUMBER: 00/336,695
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 03/899,059
PRIOR PILING DATE: 2001-09-04
PRIOR PILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 03/899,059
PRIOR PILING DATE: 2000-07-07
PRIOR RELING DATE: 2000-07-07
PRIOR RELING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR RELING DATE: 2000-07-07
PRIOR PILING DATE: 1999-05-13
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
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                                 I, Guo-Liang
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US-10-310-793-26
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US-10-279-687-8
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFILLMKSARNSCWSKDAEYGLY 240
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GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PFS50

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-10

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/293,473

PRIOR FILING DATE: 2001-06-05

PRIOR PRIOR APPLICATION NUMBER: 60/293,473
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                                                            SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                                                                                                                                                                                                                                                                                           Sequence 66, Application US/10139785
Publication No. US20030190685A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 66
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Best Local Similarity 100.
Matches 281; Conservative
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US-10-139-785-66
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US-10-310-793-26
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| Publication No. US20040005314A1 |
| Publication No. US20040005314A1 |
| GENERAL INFORMATION: |
| APPLICANT: Fox, Uddith A. |
| APPLICANT: Kalley, Sean K. |
| APPLICANT: Xiang, Hong |
| TITLE OF INVENTION HONGER: US/10/333,712 |
| CURRENT APPLICATION NUMBER: US/10/333,712 |
| CURRENT PILING DATE: 2003-01-23 |
| PRIOR PILING DATE: 2001-07-27 |
| PRIOR PILING DATE: 2000-07-27 |
| PRIOR FILING DATE: 2000-07-27 |
| NUMBER: OF SEQ ID NOS: 4 |
| SEQ ID NO 1 |
| LENGTH: 281
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                                                                                                           Query Match 100.0%; Score 281; DB 15; Best Local Similarity 100.0%; Pred. No. 6.4e-272; Matches 281; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.4e-272;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 281, Conservative
        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5
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CORGANISM: Homo Sapien
US-10-333-712-1
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Sequence 5, Application US/10292486

Publication No. US20030228309A1

GENERAL INFORMATION:

APPLICANT: Salcado et al.

FILE REPREBRENCE: PES32P1

CURRENT APPLICATION NUMBER: US/10/292,486

CURRENT FILING DATE: 2002-01-13

PRIOR PAPLICATION NUMBER: 60/433,376

PRIOR PAPLICATION NUMBER: 60/377,973

PRIOR PAPLICATION NUMBER: 60/377,973

PRIOR FILING DATE: 2001-11-14

PRIOR PRIOR PELING DATE: 2001-11-14

PRIOR PRIOR PELING DATE: 2001-11-14

PRIOR PRIOR PELING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-07

PRIOR PELING DATE: 2001-11-06

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-11-16
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FILE REFERENCE: 6255.US.C2
CURRENT APPLICATION NUMBER: US/10/279,687
CURRENT FILING DATE: 2002-10-24
FRIOR APPLICATION NUMBER: US 10/105,738
FRIOR FILING DATE: 2002-03-25
FRIOR APPLICATION NUMBER: US 09/193,663
FRIOR APPLICATION NUMBER: US 60/105,916
FRIOR APPLICATION NUMBER: US 60/065,916
FRIOR FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       US-10-279-687-8
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,431
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
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Publication No. US20040047864A1

GENERAL INFORMATION:

APPLICANT: RUDEN, Steven M

TITLE OF INVENTION: Apoptosis Inducing Molecule I

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

STREET: 9410 Key West Avenue

CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 281; DB 15; 100.0%; Pred. No. 6.4e-272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 281, Conservative
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                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                   US-10-202-062-20
                                                                                                                                                                                                                                                                                  SEQ ID NO 20
LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER EXAMPLE FURNT

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,429
FILING DATE: 16-58p-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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                           241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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LENGTH: 281 amino acids
TYPE: amino acid
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TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 281; Conservative
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                                                                                                                      US-10-662-429-2
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US-10-202-062-20
; Sequence 20, Application US/10202062
; Sequence 20, Application US/10202062
; Publication No. US2040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; FRIOR PILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.0
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FILING DATE: 13-MAR-1997
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61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                Length 281;
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JEGURACA DE CONTROL DE CONT
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100.0%; Pred. No. 6.4e-272;
tive 0; Mismatches 0;
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                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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Best Local Similarity 100.0
Matches 281; Conservative
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Best Local Similarity 100.
Matches 281; Conservative
                                       INFORMATION FOR SEQ
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MMBER: US/10/662,430
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
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Publication No. US20040048340A1
GENERAL INFORMATION:
APPLICANT Ruben, Steven M
ATTLE OF INVENTION: Apoptosis Inducing Molecule I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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STREET: 9410 Key West Avenue
CITY: Rockville
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APPLICATION MYBER: US/08/816,981
FILING DATE: 13-MA-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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                                                                                                                                                                               (301) 309-8512
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                             Length 281;
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Sequence 1, Application US/20040186051A1
GENERAL INPORMATION:
Patin INPORT F. Kelley, Stephanie H. Lindstrom
TITLE OF INVENTION: AP0-2 Ligand Variants and Uses Thereof;
FILE REFERENCE: P1858R1
CURRENT APPLICATION NUMBER: US/10/491,326
CURRENT FILING DATE: 2004-04-01
PRIOR FILING DATE: 2001-10-02
NUMBER: OF SEQ ID NOS: 6
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100.0%; Pred. No. 6.4e-272;
tive 0; Mismatches 0;
FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
FRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin Version 3.2
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-210
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ORGANISM: Homo Sapiens
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A PAPLICANT: Bristol-Myers Squibb Company; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB; TITLE OF INVENTION: PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10381160
Publication No US20040131587A1
Publication No US20040131587A1
AERIERALI INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
FILE REPERENCE: 2993-WO
CURRENT APPLICATION NUMBER: US/10/381,160
CURRENT FILING DATE: 2003-03-17
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
LENGTH: 281
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                                                                                 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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Best Local Similarity 100.
Matches 281; Conservative
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US-10-381-160-5
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US-10-755-889-210
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TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-825-282-24
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US-10-825-22

Sequence 22, Application US/10825282

Sequence 22, Application US/10825282

Sequence 22, Application No. US2004022438941

GENERAL INFORMATION:

APPLICANT: 3921-1-1-1

TITLE OF INVENTION: WETHODS FOR MAKING AND USING THE SAME

TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME

CURRENT APPLICATION NUMBER: US/10/825,282

CURRENT FILING DATE: 2004-04-14

PRIOR APPLICATION NUMBER: US/09/456,357

PRIOR FILING DATE: 1999-12-08

PRIOR APPLICATION NUMBER: 60/134,416
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Enblication No. US20040213764A1
GENERAL INFORMATION:
APPLICANT: WOLD, WILLIAM
APPLICANT: TOLLEFSON, ANN
TITLE OF INVENTION: ABBROVIRUS REPLICATION-COMPETENT VECTORS EXPRESSING
TITLE OF INVENTION: TRAIL
FILE REFERENCE: INGN:106US
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: 05/458,493
PRIOR FILING DATE: 2003-03-28
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                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 281
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Best Local Similarity 100.
Matches 281; Conservative
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US-10-810-063-2
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TITLE OF INVENTION: WIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND TITLE OF INVENTION: WETHOUS FOR MAKING AND USING THE SAME FILLE OF INVENTION: WETHOUS FOR MAKING AND USING THE SAME FILLE OF INVENTION: WETHOUS FOR MAKING AND USING THE SAME FILLE OF INVENTION: METHOUS FOR MAKING AND USING THE SAME STORENT APPLICATION NUMBER: US/10/925,282 COURRENT FILLING DATE: 1999-12-08 PRIOR FILLING DATE: 1999-12-08 PRIOR FILLING DATE: 1999-05-17 PRIOR FILLING DATE: 1999-05-17 PRIOR PELLING DATE: 1999-05-17 PRIOR PELLING DATE: 1999-05-29 PRIOR FILLING DATE: 1995-01-26 PRIOR FILLING DATE: 1995-01-26 PRIOR FILLING DATE: 1994-05-27 NUMBER OF SEQ ID NOS: 50 SOFTWARE: PARENTIN VET. 2.0
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100.0%; Score 281; DB 16;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 09/087, 195
PRIOR PTLING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 08/318,507
PRIOR FILING DATE: 1995-01-26
PRIOR APPLICATION NUMBER: 08/250,478
PRIOR FILING DATE: 1994-05-27
NUMBER: OF SEQ ID NOS: 50
SOFTWARE: PARENTIN VET. 2.0
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TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
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; ORGANISM: Homo sapiens
US-10-861-685-1
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ORGANISM: Homo sapiens
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Best Local Similarity
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Publication No. US20040247563A1
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
FILE REFERENCE: 2995-WO
CURRENT APPLICATION NUMBER: US/10/399,116
CURRENT FILING DATE: 2003-04-16
FRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 281
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Best Local Similarity 100.
Matches 281; Conservative
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US-10-399-116-5
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US-10-688-845-36
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Sequence 36, Application US/1068845; Publication No. US20040247578A1; GENERAL INFORMATION: APPLICANT: Lotze, Michael T; APPLICANT: Tahara, Hideaki

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PUDLication No. US20040253708A1
GENERAL INFORMATION:
APPLICANT: ASHRENAZI, AVI J.
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/10/861,685
CURRENT APPLICATION NUMBER: US/08/584,031
FILE REPLACED DATE: 2004-06-04
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
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FILE REFERENCE: UPT-004
CURRENT APPLICATION NUMBER: US/10/688,845
CURRENT FILING DATE: 2003-10-15
FRIOR APPLICATION NUMBER: 60/418,865
FRIOR FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
SEQ ID NO 36
LENGTH: 281
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100.0%; Pred. No. 6.4e-272;
ive 0; Mismatches 0;
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100.0%; Pred. No. 6.4e-272;
ive 0; Mismatches 0;
; FILE REFERENCE: 3802-094-27; CURRENT APPLICATION NUMBER: US/10/855,559; CURRENT FILING DATE: 2004-05-28; FRIOR APPLICATION NUMBER: US 60/475,006; PRIOR FILING DATE: 2003-06-03; NUMBER OF SEQ ID NOS: 30 SOFTWARE: PASLSEQ for Windows Version 4.0; SEQ ID NO 2; LENGTH: 281
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APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION:
FILE REFERENCE: 2966-WO
CURRENT APPLICATION NUMBER: US/10/451,200
CURRENT FILING DATE: 2003-06-21
PRIOR APPLICATION NUMBER: US 6/259,653
PRIOR PILING DATE: 2001-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 5.
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Matches 281; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapien
US-10-855-559-2
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APPLICANT: Harding, Thomas
APPLICANT: Jooss, Karin
APPLICANT: Lalant, Ashad
APPLICANT: Lonahue, Brian
TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of
TITLE OF INVENTION: One or More Anti-Angiogenic or Proapoptotic Genes
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKG 180
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100.0%; Score 281; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                             SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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APPLICANT: Flores, Heather
APPLICANT: Flores, Heather
APPLICANT: Lin, Tanya P.
APPLICANT: Lin, Tanya P.
APPLICANT: Shahrokh, Zahra
APPLICANT: Matthews, Timothy C.
TITLE OF INVENTION: AD0-2 LIGAND/TRAIL FORMULATIONS
FILE REFERENCE: P1857R1P1
CURRENT APPLICATION WUMBER: US/10/771,254
CURRENT FILING DATE: 2004-02-03
FRIOR APPLICATION NUMBER: US 60/338,249
FRIOR APPLICATION NUMBER: DCT/US02/36251
FRIOR APPLICATION NUMBER: PCT/US02/36251
FRIOR FILING DATE: 2002-11-13
FRIOR APPLICATION NUMBER: PCT/US02/36251
FRIOR SEQ ID NOS: 2
SEQ ID NO 1
FRIONT. 2002-11-12
                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10771254 Publication No. US20050020498A1 GENERAL INFORMATION:
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Publication No. US20050031593A1
GENERAL INFORMATION:
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Matches 281; Conservative
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ORGANISM: HOMO SAPIENS
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US-10-652-979-1
                                                                                                                                                                                                                                                          Best Local Similarity
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TYPE: PRT
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                                                61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                  SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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APPLICANT: FLORES, Heather
APPLICANT: LIN, Tanya P.
APPLICANT: PAI, ROGET
APPLICANT: SHAHRORH, Zahra
APPLICANT: MATTHEWS, Timothy
ITLE REPERSNCE: P1857R1
CURRENT APPLICATION NUMBER: US/10/495,353
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: PCT/US02/36251
PRIOR APPLICATION NUMBER: US 60/338,249
PRIOR PILING DATE: 2001-11-12
PRIOR PILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1.
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Publication No. US2005008958A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
TITE OF INVENTION: Apo-2 Ligand
FILE REFERENCE: P0978P3C1
CURRENT APPLICATION NUMBER: US/10/652,979
CURRENT APPLICATION NUMBER: US/05.979
PRIOR APPLICATION NUMBER: US 09/060,533
                                                                                                                                                                                                                   Sequence 1, Application US/10495353 Publication No. US20050080006A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 281; Conservative
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US-10-495-353-1
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US-10-652-979-1
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US-10-066-209-3, Application US/10066209
; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
    APPLICANT: Brigham-Burke, Michael R.
    APPLICANT: Brigham-Burke, Michael R.
    APPLICANT: Proung, Peter R.
    TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
    TITLE OF INVENTION: ANTAGONIST FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2;
    TILE REPERENCE: GH-50030-D1
; CURRENT FILING DATE: 1201-10-25
; FRIOR APPLICATION NUMBER: 09/072,993
; PRIOR PLING DATE: 1997-08-13
; PRIOR PLING DATE: 1997-08-26
; PRIOR PLING DATE: 1997-08-26
; PRIOR PLING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SUFFYARE: PASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 281; DB 17; Length 281; 100.0%; Pred. No. 6.4e-272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: US 09/007,886
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-01-08
PRIOR APPLICATION NUMBER: US 60/009,755
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
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US-09-855-544A-16
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                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 22
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                                                                                                                                                                               181 YIYSQTYFRFQEEIKENTKNDKQWVQYIYKYTSYPDPILLLMKSARNSCWSKDAEYGLYSI 240
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1 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD 60
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APPLICANT: Bermudes, G.
APPLICANT: King, I.
APPLICANT: Clairmont, C.
APPLICANT: Clairmont, C.
APPLICANT: Lin, S.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: UNMORER: US/10/738,423
CURRENT APPLICATION NUMBER: US/09/645,415
PRIOR APPLICATION NUMBER: US/09/645,415
PRIOR PILING DATE: 1099-10-04
PRIOR PILING DATE: 1999-10-04
PRIOR PILING DATE: 1999-10-04
PRIOR PILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
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                                                                                                                                                                                                                                                                                                                                                                                           241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
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Publication No. US20040229338A1
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RESULT 40

US-10-367-094-22

Sequence 22, Application US/10367094

Publication No. US20040170982A1

GENERAL INFORMATION:

APPLICANT: David W. Morris

TITLE OF INVENTION: Novel Therapeutic Targets in Cancer

FILE REFERENCE: 52945201500

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 203

SOFTWARE: PARISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 5.7e-229;
ive 0; Mismatches 0;
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100.0%; Pred. No. 3.9e-184;
iive 0; Mismatches 0;
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Patent No. US2020061525A1

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

FILE REFERENCE: 2786-0173P

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT FILING DATE: 2001-05-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 16

LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 238; Conservative
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Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-22
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ORGANISM: Homo sapiens
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Query Match 66.5%; Score 187; DB 15; L
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 187; Conservative 0; Mismatches 0;
                        PRIOR FILING DATE: 2001-02-77
PRIOR FILING DATE: 2001-02-77
PRIOR PILING DATE: 1999-05-26
PRIOR PELING DATE: 1999-05-26
PRIOR FILING DATE: 1999-05-26
PRIOR PILING DATE: 1998-11-10
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-06-29
PRIOR PELICATION NUMBER: 08/548,368
PRIOR PELICATION NUMBER: 08/548,368
PRIOR PELICATION NUMBER: 08/548,368
PRIOR PELICATION NUMBER: 08/548,368
PRIOR PELING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARCHIN VET: 2.0
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     APPLICATION NUMBER: US/09/796,581
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: synthetic fusion
US-10-652-244-13
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250 FGAFLVG 256
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67 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
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                                                                                                                                                                                                                                                         Sequence 11, Application US/10652244

Publication No. US20040052788A1

GENERAL INPORMATION:

APPLICANT: Wiley, Steven R.

APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: Cytokine that Induces Apoptosis

FILE REFERENCE: 2835-E

CURRENT APPLICATION NUMBER: US/10/652,244

CURRENT APPLICATION NUMBER: US/09/796,581

PRIOR FILING DATE: 2001-02-27

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1999-01-04

PRIOR FILING DATE: 1999-01-04

PRIOR FILING DATE: 1998-11-0

PRIOR FILING DATE: 1996-03-6

PRIOR FILING DATE: 1996-03-6

PRIOR FILING DATE: 1996-03-6

PRIOR FILING DATE: 1996-03-6

PRIOR FILING DATE: 1995-03-6

PRIOR FILING DATE: 1995-03-6

PRIOR FILING DATE: 1995-03-6

PRIOR FILING DATE: 1995-04-25

PRIOR FILING DATE: 1995-01-01

PRIOR FILING DATE: 1995-01-01
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Publication No. US20040052788A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/10/652,244
CURRENT FILING DATE: 2003-09-02
                                                                                  FYYIYSQTYFRFQ 193
                                                                                                                ; TYPE: PRT
; ORGANISM: synthetic fusion
US-10-652-244-11
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247 FGAFLVG 253
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US-10-723-003-66

Sequence 66. Application US/10723003

Publication No. US20040254108A1

GENERAL INFORMATION:
APPLICANT: WA, Jing
APPLICANT: GUO, Yajun

TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: ANTT-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003

CURRENT PILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: CN 2003101199300

PRIOR APPLICATION NUMBER: CN 2003101199300

PRIOR APPLICATION NUMBER: CN 2003-11-25

PRIOR FILING DATE: 2003-61-13

FRIOR FILING DATE: 2003-61-13

FRIOR PRIOR APPLICATION NUMBER: CN 031292909

SECTUMARE: PASESE for Windows Version 4.0

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APPLICANT: Wuest, Thomas
APPLICANT: Moosmayer, Dieter
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokir
TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
FILE REFERENCE: 1708.002US1
CURRENT APPLICATION NUMBER: US/10/389,223A
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of sequence 4: synthetic amino acid sequence of an OTHER INFORMATION: anti-body-cytokine AMAIZe fusion protein of the invention exemplif OTHER INFORMATION: TRAIL-AMAIZE (OS4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10389223A
Publication No. US20040033511A1
GENERAL INFORMATION:
APPLICANT: Fitzenmaier, Klaus
APPLICANT: Wajant, Harald
APPLICANT: Weisenwier, Thomas
APPLICANT: Woosmayer, Dieter
APPLICANT: MOOSMAY
ANAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
FITILE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
FITILE OF INVENTION OF ANTIBORY
ANTIBOR OF SEQ ID NOS: 12
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2
LENGTH: 614
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100.0%; Pred. No. 9.9e-178;
tive 0; Mismatches 0;
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100.0%; Pred. No. 8e-178;
tive 0; Mismatches 0;
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// OTHER INFORMATION: Stop codon: NT 1843-1845

US-10-389-223A-2
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; OTHER INFORMATION: Stop codon: NT 1441-1443
US-10-389-223A-4
                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 187; Conservative
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187; Conserva
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US-10-389-223A-2
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APPLICANT: Wajant, Harald
APPLICANT: Wajant, Harald
APPLICANT: Wajant, Harald
APPLICANT: Waser, Thomas
APPLICANT: Woosmayer, Dieter
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytoki
TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
FILE REFERENCE: 1708:002US1
CURRENT APPLICATION NUMBER: US/10/389,223A
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
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OTHER INFORMATION: Description of sequence 6: synthetic amino acid sequence of an OTHER INFORMATION: anti-body-cytokine AMAIZe fusion protein of the invention exempli OTHER INFORMATION: TRAIL-AMAIZE (40)
  214
                                                                                                                     274 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQWVQYIYKYT 333
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                                                                                           ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Stop codon: NT 1384-1386
US-10-389-223A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 6, Application US/10389223A; Publication No. US20040033511A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Wajant, Harald
                                                                                                                                                                                                                                                                                                              FGAFLVG 400
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Sequence 4, Application US/1085559
Publication No. US20050031593A1
GENERAL INFORMATION
APPLICANT: Harding, Thomas
APPLICANT: Lalani, Alshad
APPLICANT: Lalani, Alshad
TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of
TITLE OF INVENTION: One or More Anti-Anglogenic or Proapoptotic Genes
TITLE OF INVENTION WHERE: US/10/855,559
CURRENT FILING DATE: 2004-05-28
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 30
SOOTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                      114 VRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                     1 VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
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                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                         Length 168;
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100.0%; Pred. No. 3.9e-159;
iive 0; Mismatches 0;
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US-10-723-003-64
; Sequence 64, Application US/10723003
; Publication No. US20040254108A1
; GRNERAL INFORMATION:
; APPLICANT: MA, Jinn
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
                                                                                                                                                                       59.8%; Score 168; DB 17; 100.0%; Pred. No. 3e-159;
                                                                                                                                                                                                 Best_Local Similarity 100.0%; Pred. No. 3e-
Matches 168; Conservative 0; Mismatches
SOFTWARE: PatentIn version 3.3 SEQ ID NO 14
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Best Local Similarity 100.0
Matches 168; Conservative
                                           LENGTH: 168
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                         US-10-981-989-14
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Publication No. US20050113328A1
Publication No. US20050113328A1
Publication No. US20050113328A1
APPLICANT: INFORMATION:
APPLICANT: Devi, Gayathri
APPLICANT: Iversen, Patrick L.
APPLICANT: Iversen, Patrick L.
APPLICANT: Iversen, Patrick L.
APPLICANT: Iversen, Patrick L.
APPLICANTON: Method and Antisense Compound for Potentiating Anti-Cancer Agents
FILE REFERENCE: 50450.8058.US00
CURRENT APPLICATION NUMBER: US/10/981,989
PRIOR APPLICATION NUMBER: 60/518,139
PRIOR PILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Seol, Dae-Wu
APPLICANT: Soil, Dae-Wu
APPLICANT: Soil, Das-Wu
APPLICANT: Soiliar, Timothy R.
TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: Aboxycycline-Inducible Adeno-Associated Virus Vector, Their
TITLE OF INVENTION: Combination and Use in Gene Therapy
TITLE OF INVENTION: Combination and Use in Gene Therapy
TITLE OF INVENTION NUMBER: 2002-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR PILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
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                                                      214
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                                                                                                                                                                                                                          215 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
                                                                                                                                                                                                                                                  174 LVIHEKGFYYIYSQTYFRFQEEIKENTKONDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 233
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                         TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 60
                                                                                                                                                  488 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
                                                                                                                         155 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10, Application US/09900530A; Patent No. US20020128438A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 168; Conservative
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US-10-981-989-14
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Sequence 7, Application US/10216074

Publication No. US20030148445A1

GENERAL INFORMATION:

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: METHODS OF USE THERBOP

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT APPLICATION NUMBER: US/09/565,423

PRIOR FILING DATE: 2000-05-01

PRIOR PILING DATE: 2000-06-01

PRIOR PLING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTION VOICE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VOICE: 1000-05-01

SOFTWARE: PATENTIN VOICE: 1000-05-01

SOFTWARE: PATENTIN VOICE: 1000-05-01

SOFTWARE: PATENTIN VOICE: 1000-05-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 IHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDA 235
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     236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 2.9e-152;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                               APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TWF FAMILY
FILE REFRENCE: A-5708
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT PILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 16
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                   ; Sequence 16, Application US/09779050A; Patent No. US20020160416A1; GENERAL INFORMATION:
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Matches 161; Conservative
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Matches 166; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 233
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APPLICANT: MA, Jing
APPLICANT: GOO, Yajun
TITLE OF INVENTION: PREPRATION AND APPLICATION OF
TITLE OF INVENTION: PREPRATION AND APPLICATION OF
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REPRENCE: 54906200200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT TILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: CN 2003101199300
FRIOR APPLICATION NUMBER: CN 031292909
FRIOR PILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-10-13
SOFTWARE FABSEQ FOR Windows Version 4.0
SEQ ID NO 68
LENGTH: 582
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: CN 2003101199300
FRIOR APPLICATION NUMBER: CN 031292909
PRIOR APPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.8%; Score 168; DB 16; Length 365; 100.0%; Pred. No. 6e-159; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 9e-159;
Matches 168; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Synthetic Construct US-10-723-003-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Synthetic Construct US-10-723-003-68
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US-10-723-003-68
; Sequence 68, Application US/10723003
; Publication No. US20040254108A1
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                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 168; Conservative
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                                                                                                                        181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHLRNGELVIHEKG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11. Application US/10338083
Fublication No. US20030166559A1
GENERAL INFORMATION:
APPLICANT: Desjarlais, John R.
APPLICANT: Daniyat, Basail I.
TITLE OF INVENTION: Dominan Negative Proteins and Methods Thereof FILE REFERENCE: A-71273-2
CURRENT APPLICATION NUMBER: US/10/338,083
CURRENT FILING DATE: 2003-01-16
FRIOR APPLICATION NUMBER: US 60/345,805
FRIOR FILING DATE: 2002-01-04
FRIOR APPLICATION NUMBER: US 60/345,805
FRIOR FILING DATE: 2002-04-17
FRIOR FRIOR FILING DATE: 2002-04-17
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APPLICANT: Desjarlais, John R.
APPLICANT: Tansey, Malu Lourdes G.
APPLICANT: Tansey, Malu Lourdes G.
APPLICANT: Dabiyat. Bassil I.
TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
FILE REFERENCE: A-71273-3
CURRENT APPLICATION NUMBER: US 10/611,399
CURRENT FILING DATE: 2003-07-01
PRIOR FILING DATE: 2003-01-04
PRIOR FILING DATE: 2003-01-04
PRIOR FILING DATE: 2003-01-04
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
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Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0;
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; Sequence 11, Application US/10611399
; Publication No. US20040170602A1
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US-10-338-083-11
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US-10-338-083-11
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100.0%; Pred. No. 2.9e-152;
tive 0; Mismatches 0; Indels
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WESULY 5/
WESULY 5/
Sequence 11, Application US/10794751

Sequence 11, Application US/10794751

Sequence 11, Application US/10794751

SEMBLICANT: Thomason, Adam Read

APPLICANT: Thomason, Adam Read

PRICANT: TO INVENTION: BAFF WARIANTS AND METHODS THEREOF

PRICANT: TO INVENTION NUMBER: US/10/794,751

CURRENT FILING DATE: 2004-03-05

PRIOR APPLICATION NUMBER: US 60/482,707

PRIOR PILING DATE: 2003-01-06

PRIOR PILING DATE: 2003-01-06

PRIOR PILING DATE: 2003-11-20

PRIOR PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: US 60/523,880

PRIOR PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: US 60/523,880

PRIOR PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: US 60/523,080

PRIOR PILING DATE: 2003-11-20

PRIOR PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: US 60/528,104

PRIOR PILING DATE: 2003-11-20

SOFTWARE PALENTED NOS: 23

SOFTWARE PALENTED NOS: 23

SEQ ID NO 11

LENGTH: 161
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                                                                                                                                                                                          57.3%; Score 161; DB 16; L
100.0%; Pred. No. 2.9e-152;
tive 0; Mismatches 0;
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US-10-778-890-10
; Sequence 10, Application US/10778890
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Best Local Similarity 100.
Matches 161; Conservative
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-11
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US-10-794-751-11
                                                                                                                                                                                                                               Best Local Similarity
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us-lu-s/1-//b-5

Sequence 5, Application US/10871776

Sequence 5, Application US/10871776

Sequence 5, Application US/20040235117A1

GENERAL INFORMATION:

APPLICANT: Apotech Research and Development Ltd.

APPLICANT: Tachopp, Jurg

APPLICANT: Schneider, Pascal

APPLICANTON: Recombinant Fusion Proteins

TITLE OF INVENTION: Recombinant Fusion Proteins

TITLE OF INVENTION: NUMBER: US/10/871,776

CURRENT FILING DATE: 2002-06-28

PRIOR PILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: PCT/EP00/13032

PRIOR APPLICATION NUMBER: DE 199 63 859.4

PRIOR PILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 296

MAURING DATE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Best Local Similarity 100.0%; Pred. No. 4.8e-147;
Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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OTHER INFORMATION: mouseACRF30 as 18-111
FEATURE:
                                                                                                                                               LOCATION: (17)...(108)
OTHER INFORMATION: mouseACRP30 aa 18-111
EASTIORE: DOMAIN
LOCATION: (109)...(110)
OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: DOMAIN
COCATION: (111)...(296)
COTHER INFORMATION: humanTRAIL aa 95-281
US-10-185-425-5
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                               OTHER INFORMATION: Linker FEATURE:
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NAME/KEY: DOMAIN
LOCATION: (9)...(16)
OTHER INFORMATION: Linker
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OTHER INFORMATION: Flag
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NAME/KEY: DOMAIN
LOCATION: (1)...(
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APPLICANT: Apotech Research and Development Ltd.
APPLICANT: Techopp, Jurg
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Holler, Nila
TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
TITLE OF INVENTION NUMBER: US/10/185,425
CURRENT APPLICATION NUMBER: US/10/185,425
PRIOR APPLICATION NUMBER: DET/FP00/13032
PRIOR APPLICATION NUMBER: DE 199 63 859.4
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSI 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
PUDLication No. US20050112596A1
GENERAL INFORMATION:
APPLICANT: TSCHOPP, JUNG
TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WITH GROWTH EFFECTS
FILE REFERENCE: A049 US
CURRENT FILING DATE: 2004-02-12
CURRENT APPLICATION NUMBER: US/09/520,489
PRIOR APPLICATION NUMBER: US/09/520,489
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-12
PRIOR FILING DATE: 1998-09-12
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 10
LENGTH: 158
THOS BELIAND AND THE NOS: 16
SEQ ID NO 10
LENGTH: 158
THENCH STATES THENCH STATES THENCH THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
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OTHER INFORMATION: TRAIL-ACRP30
FEATURE:
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ORGANISM: Artificial Sequence
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LOCATION: (1)...(8)
OTHER INFORMATION: Flag
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NAME/KEY: DOMAIN
LOCATION: (9)...(16)
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LENGTH: 296
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 246
                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-855-544A-13
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ORGANISM: Homo sapiens
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US-10-978-203-23
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LENGTH: 271
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                                                                                                                                                                     Similarity 100.0%; Score 156; DB 16; Length 2 Similarity 100.0%; Pred. No. 4.8e-147; S6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SAVITZKY et al.,
TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS:
FILE REFERENCE: 2786-0151P
CURRENT APPLICATION NUMBER: US/10/781,866
CURRENT FILING DATE: 2004-02-20
PRIOR PLING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 29
LENGTH: 169
                                                                                                                                                                                                                                                                                                                                                                                                                          261 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 296
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Batent No. US20020061525A1

GENERAL INFORMATION:
APPLICANT: ROGATION SEQUENCES OF TRAIL VARIANTS
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
                                                                        NAME/KEY: DOMAIN
COCATION: (111)...(296)
COTHER INFORMATION: humanTRAIL as 95-281
US-10-871-776-5
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US-10-781-866-29
Faquence 29, Application US/10781866
Publication No. US20040258681A1
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Best Local Similarity 100.C
Matches 141; Conservative
                                                                                                                                                                                                           Matches 156; Conservative
                   LOCATION: (109)...(110)
OTHER INFORMATION: Linker
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US-10-781-866-29
 NAME/KEY: DOMAIN
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Best Local
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                                                                                                      141 SKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEBIKENT
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Length 246;
                                                   0; Indels
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Publication No. US20050112666A1
GENERAL INFORMATION:
APPLICANT: Chicheportiche, Yves
APPLICANT: Browning, Jeffrey
TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand
FILE REFERENCE: A003
CURRENT APPLICATION NUMBER: US/10/978,203
CURRENT PILING DATE: 2004-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-781-866-30

Sequence 30, Application US/10781866

Publication No. US20040258681A1

GENERAL INFORMATION:

APPLICANT: SAVITZKY et al.

TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS

FILE REFERENCE: 2786-0151P

CURRENT PELLICATION NUMBER: US/10/781,866

CURRENT FILING DATE: 2004-02-20

PRIOR APPLICATION NUMBER: US/09/569,611

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver. 2.0
50.2%; Score 141; DB 9; Le
100.0%; Pred. No. 3.9e-132;
tive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 141; Conservative
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Sequence 29, Application US/10959537; Publication No. US20050069983A1; GENERAL INFORMATION:
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US-10-116-378-29
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ORGANISM: Homo sapiens
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Matches 127, Conserva
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46.3%; Score 130; DB 17; L
Best Local Similarity 100.0%; Pred. No. 4.3e-121;
Matches 130; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/023,541
PRIOR FILING DATE: 1996-08-07
PRIOR FILING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: 60/040,820
PRIOR APPLICATION NUMBER: 60/040,820
PRIOR FILING DATE: 1997-03-18
NUMBER OF FILING DA
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Best Local Similarity 100.0
Matches 130; Conservative
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CAGANISM: homo sapien
US-10-978-203-23
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US-10-978-131-23
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                             SEQ ID NO 23
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Gunda, Audrey
APPLICANT: Gunday, Audrey
APPLICANT: Gunday, Audrey
APPLICANT: Gunday, Auglin
APPLICANT: Wood, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
TITLE OF INVENTION: NOVEL TUMOR THE SAME
FILE REFRENCE: Pl206R1
CURRENT APPLICATION NUMBER: US/10/959,537
CURRENT FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US/02/47,225
PRIOR APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
LENGTH: 164
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Sequence 29, Application US/10116378

| Sequence 29, Application US/10116378
| Publication No. US20020150993A1
| GENERAL INFORMATION:
| APPLICANT: Ashkenazi, Avi J.
| APPLICANT: Gurney, Austin
| APPLICANT: Margers, Scot A.
| APPLICANT: Mood, William
| APPLICANT: Pitti, Robert M.
| APPLICANT: Pitti, Robert M.
| APPLICANT: Pitti, Robert M.
| APPLICANT: Wood, William
| TITLE OF INVENTION: NOVELET THOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
| TITLE OF INVENTION: NOVELET
| TITLE OF INVENTION: ACIDS ENCODING THE SAME
| FILE REFERENCE: Pl206R1
| FILE REFERENCE: Pl206R1
| CURRENT FILING DATE: EARLIER FILING DATE: 1999-02-09
| PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-09
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
| SEQ ID NOS: 31
| LENGTH: 164
| LENGTH: 164
| LENGTH: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.2%; Score 127; DB 13; L ilarity 100.0%; Pred. No. 2.7e-118; Conservative 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                     US-09-855-544A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 14
LENGTH: 188
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LENGTH: 98
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                                                                                                                                                          178 EKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 237
                                                                                                                                                                                     61 EKGFYYIYSQTYFRFQEEIKENTKUDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY 120
                                                                                          1 GPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa , OTHER INFORMATION: polypeptide encoded by the DNA sequence of SEQ ID NO:4 US-10-006-305A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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                                                                     118 GPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH
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                          Indels
Best Local Similarity 100.0%; Pred. No. 2.7e-118; Matches 127; Conservative 0; Mismatches 0;
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Patent No. US20020061525A1

GENERAL INFORMATION:

APPLICANT: Redrigo YELIN et al.

TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT PILING DATE: 2001-05-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1
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Sequence 8, Application US/10006305A

Publication No. US20050048476A1

GENERAL INFORMATION

GENERAL INFORMATION

THUR OF INVENTION NOVEL CHIMERIC TNF LIGANDS

TITLE OF INVENTION NOVEL CHIMERIC TNF LIGANDS

TITLE OF INVENTION NOVEL CHIMERIC TNF LIGANDS

CURRENT APPLICATION NUMBER: US/10/006,305A

CURRENT APPLICATION NUMBER: US/10/006,305A

CURRENT FILING DATE: 2001-12-06

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: PATCHIN VET: 3.2

SOFTWARE: PATCHIN VET: 3.2
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                                                                                                                                                                                                                                                       238 GLYSIYQ 244
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US-09-855-544A-15
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                                                                                                   61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQ 107
                                                                                                                                               61 DDSYWDPNDEBSWNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQ 107
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                                                                                                                                                                                                                                                                        Sequence 14, Application US/09855544A
Fatent No. US20020061525A1
GENERAL INPORMATION:
APPLICANT: ROATIGO YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT APPLICATION DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOOTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 1.5e-81;
tive 0; Mismatches 0;
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Patent No. US20020061525A1

GENERAL INFORMATION:
APPLICATIVE ROGATION SEQUENCES OF TRAIL VARIANTS

TILLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P

CURRENT APPLICATION NUMBER: US/09/855,544A

CURRENT FILING DATE: 2001-05-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 100.
Matches 90; Conservative
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
                                                                                                                                                                       GENERAL INFORMATION
                                                                                                        US-10-781-866-32
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      Sequence 20, Application US/10367094

Publication No. US20040170982A1

GENERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: Macc Malandro

ITTLE OF INVENTION: Novel Therapeutic Targets in Cancer

FILE REFERENCE: 529452001500

CURRENT APPLICATION NUMBER: US/10/367,094

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 203

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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| Sequence 4, Application US/10652244
| Publication No. US20040052788A1
| GENERAL INFORMATION:
| APPLICANT: Wiley, Steven R.
| CURRENT APPLICATION: Cytokine that Induces Apoptosis FILE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E 2003-09-02
| PRIOR PELING DATE: 2001-02-27
| PRIOR PILING DATE: 1999-05-26
| PRIOR PELING DATE: 1999-05-26
| PRIOR PRILING DATE: 1998-11-10
| PRIOR PILING DATE: 1998-11-10
| PRIOR PILING DATE: 1998-06-25
| PRIOR PILING DATE: 1996-06-25
| PRIOR FILING DATE: 1996-06-25
| PRIOR FILING DATE: 1995-06-25
| PRIOR FILING DATE: 1995-06-29
| PRIOR FILING DATE: 1995-06-29
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100.0%; Pred. No. ...
0; Mismatches
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Best Local Similarity 100.
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-20
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Best Local Similarity
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US-10-652-244-4
US-10-367-094-20
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

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100.0%; Pred. No. 1.9e-81;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.0%; Score 90; DB 16; Length 12 Best Local Similarity 100.0%; Pred. No. 1.8e-81; Matches 90; Conservative 0; Mismatches 0; Indels
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Sequence 31, Application US/10781866

Publication No. US20040258681A1

Sequence 31, Application US/10781866

Publication No. US20040258681A1

TELE OF INVENTION: ALTERNATIVE SPLICING VARIANTS

TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS

CURRENT APPLICATION NUMBER: US/10/781,866

CURRENT PILING DATE: 2004-02-20

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 31
                                                                    APPLICANT: SAVITZKY et al.
TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
FILE REFERENCE: 2786-0151P
CURRENT APPLICATION NUMBER: US/10/781,866
CURRENT FILING DATE: 2004-02-20
PRIOR PLING DATE: 2000-05-10
PRIOR PLING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 32
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 DDSYMDPNDEESMNSPCWQVKWQLRQLVRK 114
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Sequence 32, Application US/10781866 Publication No. US20040258681A1
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Best Local Similarity 100.
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-10-781-866-31
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12, Appl 6479, Ap 13, Appl 8, Appl 8, Appl 6, Appl 13, Appl 14513, A 14513, A 15559, Ap 5559, Ap 5559, Ap 55649, Ap 64, Appl 2, Appl

Perfect score: Sequence: Scoring table:

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Word size :

Searched:

Minimum DB 8 Maximum DB 8

Database :

Result No.

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US-09-105-34A-6

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US-09-105-24A-14513

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US-09-105-24A-14513

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US-09-107-268-189

US-09-107-268-199

US-09-107-270-767-299

US-09-107-270-767-299

US-09-270-767-299

US-09-270-767-2994

US-09-270-767-39444

US-09-270-767-3644
                                5-09-569-611C-31
5-09-632-287A-12
5-09-621-976-6479
5-09-628-665-14
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6, Appli
11, Appli
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(without alignments)
499.438 Million cell updates/sec
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Sequence 1,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ReCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-584-031-1

US-08-883-086-1

US-09-333-086-10

US-09-333-584-1

US-09-333-583-2

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-918-039-118

US-09-072-993C-3

US-09-320-424-11

US-09-320-424-11

US-09-320-424-13

US-09-569-611C-29

US-09-569-611C-29

US-09-569-611C-29

US-09-569-611C-29

US-09-569-611C-29

US-09-569-611C-29

US-09-569-611C-30

US-09-559-611C-30
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Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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186, App 1189, App 1189, App 11821, Ap 11821, App 11022, App 1103, App 60, App 1179, A

99, Appl 8267, Ap 4, Appli 4, Appli 4, Appli

10, Appl 4, Appli 4, Appli

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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
                                                                                                                                                                                           GENERAL INCORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669-220803
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SQU ID NO I
LENGTH: 281
                                                                                                          RESULT 2
18-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                               ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                        Sequence 2, Application US/08670354
Patent No. 576323
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIPETATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acids TYPE: amino acid
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COUNTRY: U
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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; Patent No. 6046048
; GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTON: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE Genenteck, Inc.
; STREET: 460 Point San Bruno Blvd
; STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
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                           241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Pred. No. 6e-279;
iive 0; Mismatches 0;
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181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                                                                                                                                                                                                                                             100.0%; Score 281; DB 3; Length 281; 100.0%; Pred. No. 6e-279; tive 0; Mismatches 0; Indel8
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JAPPLICANT: Goodwin, Raymond G.
JITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT APPLICATION NUMBER: US/190,046
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1996-06-25
EARLIER PILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER PILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENT VOR: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09320424; Patent No. 6284236
                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
TYPE: amino acid
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Matches 281, Conservative
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Matches 281; Conservative
              TELEPHONE: 847-937-03
TELEFAX: 847-938-2623
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ORGANISM: human
                                                                                                                                                                                                                                                   US-08-883-086-10
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Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: POR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                       Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                  Score 281; DB 3;
Pred. No. 6e-279;
                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 281; Dr
Best Local Similarity 100.0%; Pred. No. 6e-
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ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PSACESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,086
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STREET: 100 Abbott Park Road
CITY: Abbott Park
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 90978
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/225-5416
TELEFAX: 415/352-9881
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
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ATTORNEY/AGENT INFORMATION:
NAME: POTEMBEK!, Priscilla B.
REGISTRATION NUMBER: 33,207
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TELECOMMUNICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-883-086-10
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPQ 120
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                     Sequence 11, Application US/09157864

Patent No. 6440694

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Biantowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Mills, Cynthia J
APPLICANT: TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
ADDRESSEE: Legal Services
STREET: 30. Henrietta Street
CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 281; DB 4; 100.0%; Pred. No. 6e-279;
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TELECOMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
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; Patent No. 6521228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 616/833 8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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STATE: MI
COUNTRY: U
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Best Local
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                               61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                                                       PYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                    121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 60
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APPLICANT: YOUNG, PETER R.
APPLICANT: MASSHALL, LISA A.
APPLICANT: MASSHALL, LISA A.
APPLICANT: MASSHALL, LISA A.
APPLICANT: TAN, KONG B.
APPLICANT: TAN, KONG B.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR, TITLE OF INVENTION: TROS NECROSIS FACTOR RELATED RECEPTOR, TITLE OF INVENTION: TWO RECORDS.
TITLE OF INVENTION: TWO NECROSIS FACTOR RELATED RECEPTOR, TITLE OF INVENTION: TOWN NECROSIS FACTOR RELATED RECEPTOR, TITLE OF INVENTION: UNMBER: U8/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR PILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 3.0
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100.0%; Score 281; DB 3;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09333593A Patent No. 6313269 GENERAL INFORMATION:
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; ORGANISM: HOMO SAPIENS
US-09-333-593A-6
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                                      100.0%; Score 281; DB 4; Length 281; 100.0%; Pred. No. 6e-279; ive 0; Mismatches 0; Indels
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APPLICANT: Kelley, Robert F.
APPLICANT: Cornell, Mark P.
APPLICANT: O'COMENI, Mark P.
APPLICANT: Schwall, Ralph H.
TITLE OF INVENTION: Apo-2 Ligand
TITLE OF INVENTION: Apo-2 Ligand
CURRENT APPLICATION NUMBER: US/09/582,450
CURRENT FILING DATE: 2001-05-14
PRIOR PILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-01-15
SEQ ID NO: 1
LENGTH: 281
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                                                                 cal Similarity 100.
281; Conservative
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US-09-582-450-1
US-09-919-039-118
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                                           Query Match
Best Local Si
Matches 281
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Sequence 118, Application US/09919039

Sequence 118, Application US/09919039

Sequence 118, Application US/09919039

Patent No. 672-1066

GENERAL INFORMATION:
TILE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES TITLE OF INVENTION: BALO35 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 118

LENGTH: 281
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            APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
ITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR PELING DATE: 1999-05-26
PRIOR PELING DATE: 1999-05-26
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 09/670,354
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR RELING DATE: 1995-06-29
PRIOR PELING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARR: PATENTIN VET: 2.0
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
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Best Local Similarity 100.
Matches 281; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: human
US-09-825-563-2
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  1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis'
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                               241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UNN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 587-0430
(206) 233-0644
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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100.0%; Score 281; DB 4;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 281; DB 4;
Pred. No. 6e-279;
0; Mismatches 0;
                                                                                              US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 674668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22033
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR PILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1.
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TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10011125A Patent No. 6828121
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Best Local Similarity 100.0%;
Matches 281; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-09-934-465-1
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275 FGAFLVG 281
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APPLICANT: Michael R. Brigham-Burke
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Michael R. Brigham-Burke
APPLICANT: MICHAEL R. Brigham-Burke
APPLICANT: MICHAEL R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: A MATAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
TITLE OF INVENTION: A MATAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
TITLE OF INVENTION: A MATAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
TILLE OF INVENTION: 1999-05-06
CURRENT FILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/055,550
PRIOR APPLICATION NUMBER: 60/055,550
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGT: 279
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                    FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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US-09-320-424-11
; Sequence 11, Application US/09320424
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US-09-072-993C-3
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127 ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 186
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woley, Steven R.
APPLICANT: Woley, Steven R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2813-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER APPLICATION NUMBER: 08/546
EARLIER PILING DATE: 1998-03-26
EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-10-01
EARLIER FILING DATE: 1995-10-01
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOWER: 08/496,632
ILENGTH: 253
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APPLICANT: Wiley, Steven R.

APPLICANT: Wiley, Steven R.

TITES OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E

CURRENT APPLICATION NUMBER: US/09/825,563

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: 09/190,046

PRIOR APPLICATION NUMBER: 09/190,046

PRIOR PILING DATE: 1999-05-26

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1995-11-01

PRIOR FILING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0
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Patent No. 6521228
GENERAL INFORMATION:
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; ORGANISM: synthetic fusion
US-09-320-424-11
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190 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249
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Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: POR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 256;
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Sequence 13, Application US/0982563

Sequence 13, Application US/0982563

Sequence 13, Application US/0982563

Sequence 13, Application US/0982563

GENERAL INFORMATION:

APPLICANT: Goodwin, Raymond G.

TITLE OF INVENTION: CYtokine that Induces Apoptosis

FILE REFERENCE: 2835-E

CURRENT APPLICATION NUMBER: US/09/825,563

CURRENT FILING DATE: 1999-05-26

PRIOR PILING DATE: 1999-05-26

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: 09/046

PRIOR APPLICATION NUMBER: 09/046

PRIOR FILING DATE: 1998-01-06

PRIOR FILING DATE: 1996-06-25

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-29

NUMBER: 08/10 NOS: 25

SEQ ID NOS: 25

LENGHALL: 256
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STREET: 100 Abbott Laboratories
CITY: Abbott Park Road
CITY: Abbott Park
STATE: 1L
COUNTRY: US*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: synthetic fusion
US-09-825-563-13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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250 FGAFLVG 256
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                                                                                                                                                                                                                                                                                                                                                                                187 SYPOPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249
                                                                                                                                                                                                                                                                        67 TSEETISTYQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126
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                                                                                                                                                                                                                                          95 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                                                                                                                                                                                                                                                  ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
                                                                                                                                                                                        Gaps
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                                                                                                                                 Query Match 66.5%; Score 187; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 6.4e-183; Matches 187; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/046, 641
EARLIER PELLING DATE: 1998-11-10
EARLIER PELLING DATE: 1998-03-26
EARLIER PELLON NUMBER: 08/670, 354
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1995-06-25
EARLIER FILING DATE: 1995-06-25
EARLIER FILING DATE: 1995-06-25
EARLIER FILING DATE: 1995-06-25
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHTIN VOWER: 08/548, 368
EARLIER FILING DATE: 1995-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09320424
Patent No. 6284236
                        ; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-13
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247 FGAFLVG 253
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LENGTH: 256
LENGTH: 253
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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 PLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 PLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRN 171
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           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                      121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
                                                                                                                                           241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SAVITZKY et al.
TITLE OF INVENTION:
FILE REFRENCE: 2786-0151P;
CURRENT APPLICATION NUMBER: US/09/569,611C
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 29
LENGTH: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.2%; Score 141; DB 4; Le
100.0%; Pred. No. 4.6e-136;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SAVITEKY et al.
APPLICANT: SAVITEKY et al.
TILLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
FILE REFERENCE: 2786-0151P
CURRENT APPLICATION NUMBER: US/09/569,611C
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 4;
Pred. No. 1e-128;
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                                                                                                                                                                                                                                                                                        Sequence 29, Application US/09569611C Patent No. 6720182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 RVAAHITGTRGRSNTLSSPNS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09569611C
Patent No. 6720182
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Best Local Similarity 100.
Matches 141; Conservative
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Best Local Similarity 100.
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-569-611C-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30
                                                                                                                                                                                                                                                                           US-09-569-611C-29
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TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 10999-05-06
PRIOR FILING DATE: 1999-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 SNLHLRNGELVIHEKGFYXIYSQTYFRFQEEIKENTKODKQMVQYIYKYTSYPDFILLMK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 174; DB 3; Length 177;
Pred. No. 9e-170;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
APLORNEY DATE: 12-FEB-1998
ATTORNEY AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09565423; Patent No. 6475987; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: No. 6207642e
                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 177 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100. Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 177 amino acid
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US-09-565-423-7
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SOFTWARE: Patentin Ve
SEQ ID NO 7
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Query Match
Best Local Similarity
       SOFTWARE:
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Sequence 7833, Application US/09513999C

RECENT NO. 6783961

SENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENT APPLICATION NUMBER: US 60/122,487

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
182 GELVIHEKGFYYIYSQTYFRFQEEIKENTKADKQMVQYIYKYTSYPDFILLMKSARNSCW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 CVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08670354;
Sequence 4, Application US/08670354;
Patent No. 576323;
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALDRESSE:
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: -32.,-1
OTHER INFORMATION: SCORE 5.3
OTHER INFORMATION: SEQ VIFTVLLQSLCVA/VT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: Apple Macincosh
OPERATING SYSTEM: Apple 7.5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: -18
; OTHER INFORMATION: Xaa=Asn or Thr
US-09-513-999C-7833
                                                                                                      242 SKDAEYGLYSIYQG 255
                                                                           232 SKDAEYGLYSIYQG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: -18
                                                                                                                                                                                                                         US-09-513-999C-7833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7833
LENGTH: 121
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Sequence 4, Application US/09320424

Patent No. 6284236

GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Geodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E
CURRENT FALLING DATE: 1999-05-26
EARLIER PELICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-03-26
EARLIER PELICATION NUMBER: 09/648,641
EARLIER PELICATION NUMBER: 08/670,354
EARLIER PELICATION NUMBER: 08/670,354
EARLIER PELICATION NUMBER: 08/50,632
EARLIER PELICATION NUMBER: 08/50,632
EARLIER PELING DATE: 1995-10-01
EARLIER FILING DATE: 1995-10-01
EARLIER PELING DATE: 1995-06-29

NUMBER OF SEQ ID NOS: 25

SEQ ID NOS: 25

LENGTH: 101
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Pred. No. 3.9e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.0%; Score 90; DB 1; Le
100.0%; Pred. No. 3.9e-84;
tive 0; Mismatches 0;
Microsoft Word, Version 6.0.1
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                                    CURRENT AFFLICATION NUMBER: US/08/670,354
PILING DATE: 25-UNA-1996
CLASSIFICATION ATA:
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UNA-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERNEK/DOCKET NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERNEK/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-4330:
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 90; Conservative
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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ORGANISM: human
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                                                                             1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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       Gaps
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       Indels
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kethryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                            APPLICANT: Wiley, Steven R. APPLICANT: Wiley, Steven R. APPLICANT: Goodwin, Raymond G. TITLE OF INVENTION: Cytokine that Induces Apoptosis FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.0%; Scor.
100.0%; Pred. No.
     Mismatches
                                                                                                                      61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
                                                                                                                                          61 DDSYWDPNDEESWNSPCWQVKWQLRQLVRK 90
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CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR FILING DATE: 1999-05-26
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/670,354
PRIOR FILING DATE: 1995-06-25
PRIOR APPLICATION NUMBER: 08/670,368
PRIOR FILING DATE: 1995-06-29
PRIOR APPLICATION NUMBER: 08/496,632
PRIOR APPLICATION NUMBER: 08/496,632
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                     ; Sequence 4, Application US/09825563; Patent No. 6521228; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
     Conservative
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Best Local Similarity 100.
Matches 90; Conservative
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ORGANISM: human
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ZIP: 98101
     90;
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Matches"
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25 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 84
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3.9e-84;
hes 0; Indels
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Fatent No. 6720182
GENERAL INFORMATION:
FILLE APPLICANT: SAVITZKY et al.
FILLE REFRENCE: 2786-0151P
CURRENT PELLIGN NUMBER: US/09/569,611C
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 32
LENGTH: 120
TENGTH: 120
TENGTH: 120
CRANISM: Homo sapiens
US-09-569-611C-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.0%; Score 90; DB 100.0%; Pred. No. 3.9 tive 0; Mismatches
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Microsoft Word, Version 6.0.1
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                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANGEREOR, KALPYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT ON INFORMATION:
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT ON INFORMATION:
ARTHREVARIATION INFORMATION:
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ARTHREVARIATION INFORMATION:
ARTHREVARIATION INFORMATION:
                                               APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 90; Conservative
                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.0
Best Local Similarity 100.
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein PCT-US96-10895-4
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US-09-569-611C-32
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; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-14
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Patent NO. 6673771

GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Minosaki, Masahiko
TILE OF INVENTION: Methods of Inhibiting Osteoclast Activity
FILE PEREBUCE: UPN3831
CURRENT APPLICATION NUMBER: US/09/628,665
CURRENT PILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 24; DB 4; Length 59; 100.0%; Pred. No. 6.9e-17; ive 0; Mismatches 0; Indels
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5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels
                 TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENEET. 05.PR2
CURRENT APPLICATION WINBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6479
LENGTH: 59
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                                                                                                                                                                                                                                                                                NAME/KEY: UNSURE
LOCATION: 27
OTHER INFORMATION: Xaa = Glu,Gln
MAME/KEY: UNSURE
LOCATION: 34
OTHER INFORMATION: Xaa = Glu,Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 33,57
OTHER INFORMATION: Xaa = Leu,Pro
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 25,32
OTHER INFORMATION: Xaa = Leu, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 RFQEEIKENTKNDKQ 205
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 15
    Giordano, J.Y.
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
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US-09-628-665-32
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Best Local Si
Matches 24;
APPLICANT:
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Sequence 12, Application US/09632287A

Patent No. 6521422

GENERAL INFORMATION:
APPLICANT: How, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 01017/33550A

CURRENT FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/147,294

PRIOR APPLICATION NUMBER: US 60/147,294

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.0%; Score 90; DB 4; Length 122; Best Local Similarity 100.0%; Pred. No. 4.6e-84; Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.2%; Score 85; DB 4; Length 85; Best Local Similarity 100.0%; Pred. No. 4.3e-79; Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                     GENERAL INFORMATION:

APPLICANT: SAVITEKY et al.

ITILE OF INVENTION: ALTERNATIVE SPLICING VARIANTS;
FILLE REFERENCE: 2786-0151P;
CURRENT APPLICATION NUMBER: US/09/569,611C

CURRENT FILLE DATE: 2000-05-10

NUMBER OF SQU ID NOS: 52

SOFTWARE: PATENT VET. 2.0

SEQ ID NO 31

LENGTH: 122

ILENGTH: 122

TYPE: PRF: PRF: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDSYMDPNDEESMNSPCWQVKWQLRQLVRK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 IHEKGFYYIYSQTYFRFQEEIKENT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IHEKGFYYIYSQTYFRFQEEIKENT 85
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                                            ; Sequence 31, Application US/09569611C ; Patent No. 6720182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-632-287A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
US-09-621-976-6479
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US-09-632-287A-12
                                                                                                                                                                                                                                                                                                                                                                                US-09-569-611C-31
                        JS-09-569-611C-31
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Query Match 5.0%; Score 14; DB 3; Length 183; Best Local Similarity 100.0%; Pred. No. 3.1e-06; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESSPONDENCE ADDRESS: ADDRESSEE Rathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14; DB 1; Lo
Pred. No. 4.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-UW-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UUN-1995
CLASSTRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2835-B
                                                                                                                                                                                                                             US-08-670-354-6
; Sequence 6, Application US/08670354
; Patent No. 576323
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Sequence 6, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 5.0%; SC Local Similarity 100.0%; P les 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                207 VOYIXKYTSYPDPI 220
                                                                                                                         109 VQYIYKYTSYPDPI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 VQYIYKYTSYPDPI 230
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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STATE:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Kinosaki, Masahiko
TITLE OF INVENTON: Methods of Inhibiting Osteoclast Activity
FILE REFERENCE: UPN3831
CURRENT APPLICATION NUMBER: US/09/628,665
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,094
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: POR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDACT LARK Road
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%; Score 15; DB 4; Length 19;
100.0%; Pred. No. 3.9e-08;
tive 0; Mismatches 0; Indele
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COMPUTRY: 1L
COMPUTRY: 1USA
COMPUTER: EDSABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSED for Windows
SOFTWARE: 12-FBH: WINDOWS VERSION 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FBB-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FBB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryll L. REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,412
TELEPHONE: 847-938-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 8, Application US/09105343A; Patent No. 6207642
                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 RFQEEIKENTKNDKQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: No. 6207642e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RFQEEIKENTKNDKQ 17
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LENGTH: 183 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 15; Conservative
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TOPOLOGY: linear
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US-09-105-343A-8
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COUNTRY:
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
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Best Local Similarity 100.u
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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US-09-632-287A-13
                                                                                                                                                                                                                                                                                                                                                                                         STATE: WA
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    PCT-US96-10895-6
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Pred. No. 4.7e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
Goodwin, Raymond G.
NVENTION: Cytokine that Induces Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7e-06;
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                            TITLE OF INVENTION: Cytckine that Induces Apprile REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT PILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER PILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1995-06-29
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARENTING DATE: 1995-06-39
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARENTING DATE: 1995-06-39
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE MEREKENELS: 423-5

CURRENT APPLICATION NUMBER: US/09/825,563

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: 09/320,424

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1998-11-10

PRIOR FILING DATE: 1998-03-26

PRIOR PLICATION NUMBER: 09/048,641

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 1995-11-01

PRIOR APPLICATION NUMBER: 08/540,368

PRIOR PELING DATE: 1995-11-01

PRIOR APPLICATION NUMBER: 08/546,368

PRIOR FILING DATE: 1995-11-01

PRIOR FILING DATE: 1995-10-01

PRIOR FILING DATE: 1995-10-02

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PALENTIN VET: 2.0
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14 '$0.001
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; Patent No. 6521228
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Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: murine US-09-320-424-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: murine
US-09-825-563-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-825-563-6
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RESULT 38

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PRESENTATION OF THE PROPERTY O
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192 FQEEIKE 198
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                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 QEEIKEN 15
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SILVEN, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiggard, Wogger, C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
FILE REFERENCE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14513
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MCDONALD, PETER J
APPLICANT: JOHNSON, ALAN M
TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND
TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                  Gaps
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                                                         4.3%; Score 12; DB 4; Length 87;
100.0%; Pred. No. 0.00018;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 70;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,481
FILING DATE: 12-APR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: INTERNATIONAL PCT/AU91/00347
FILING DATE: 09-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: BILD GATEHOUSE ROAD
CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Scc.
v 100.0%; Pred. No. --
                                                                                                                                                                                                                                                                           ; Sequence 14513, Application US/09902540
; Patent NO. 683147
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-972-481-2; Sequence 2, Application US/07972481; Patent No. 557843; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14513
                                                     Query Match
Best Local Similarity 100.
                                                                                                                                       183 YIYSQTYFRFQE 194
                                                                                                                                                              65 YIYSQTYFRFQE 76
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
; ORGANISM: Mouse
US-09-632-287A-13
                                                                                                                                                                                                                                      RESULT 40
US-09-902-540-14513
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RESULT 42
US-09-513-999C-5589
; Sequence 5589, Application US/09513999C
; Patent No. 678361
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 678361
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1909-02-24
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5589
; LENGTH: 132
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Sequence 5590, Application US/09513999C

Patent No. 6783961

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PILE REFERENCE: 59.US2.REG

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C
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Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.5%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches
NAME: SVENSSON, LECNARD R
REGISTRATION NUMBER: 30,330
REFERENCE, FOCKET NUMBER: 446-102PCT
TELECOMMINICATION INPORMATION:
TELEPAX: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: UNSURE
LOCATION: 116
OTHER INFORMATION: Xaa=Ala or Asp or Glu
US-09-513-999C-5589
                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-07-972-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                    Length 172;
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                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8 Application US/09096724B
Fatent No. 6548290
GENERAL INFORMATION:
APPLICANT: MCGAITY, Thomas J.
APPLICANT: KISCHNEY, MARC M.
TITLE OF INVENTION: Geminin Gene and Protein
FILE REFERENCE: 0725.1055-001
CURRENT APPLICATION NUMBER: US/09/096,724B
CURRENT APPLICATION NUMBER: US/09/096,724B
CURRENT APPLICATION NUMBER: US/09/096,724B
CURRENT APPLICATION NUMBER: 05/085,371
FRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FattSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24. Application US/09096724B
Sequence 10. 6548290
Sequence 10. 6548290
Sequence 24. Application US/09096724B
Sequence 10. 6548290
Sequence 10. 6549290
Sequence 10. 6549
                                                                                                                                                                                                                                    2.5%; Score 7; DB 3;
100.0%; Pred. No. 42;
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                               ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5649
      PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                              NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5649
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                      272 ASFFGAF 278
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                                                                                                                                                                                                                                                                                                                                                                                                      105 ASFFGAF 111
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 47
US-09-096-724B-24
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US-09-096-724B-8
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BFIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BFIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: US 60/64,964
PRIOR PILING DATE: 1997-11-08
PRIOR PLING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/655,779
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US-09-513-999C-5591
Sequence 5591, Application US/09513999C
Patent No. 678361
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION:
Patent No. 6783961
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.U32.REG
CURRENT FILING DATE: 200-02-24
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5591
LEMCTH: 132
LEMCTH: 132
LEMCTH: 132
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                                                                                                                                                                                                                                                                                                                                                                                                         2.5%; Score 7; DB 4;
100.0%; Pred. No. 33;
vative 0; Mismatches
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100.0%; Pred. No. 33;
tive 0; Mismatches
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; OTHER INFORMATION: Xaa=Ala or Asp or Glu
US-09-513-999C-5591
                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Xaa=Ala or Asp or Glu
US-09-513-999C-5590
PRIOR APPLICATION NUMBER: US 60/122,487 BYOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                         NAME/KEY: UNSURE LOCATION: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: UNSURE
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US-09-134-001C-5649
                                                                                                                  SEQ ID NO 5590
LENGTH: 132
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US-09-270-767-50664

Sequence 50664, Application US/09270767

Sequence 50664, Application US/09270767

Sequence 50664, Application US/09270767

SERNEAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

NULleic acids and proteins of Drosophila melanogaster FILE REFRENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

SOUTHEN PETENT PILING PATE: 1999-03-17

SOUTHEN PETENT VETENT V
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
LENGTH: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.5%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches
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US-09-302-626B-186
i Sequence 186, Application US/09302626B
; Pactent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Rappuoli, Rio
APPLICANT: Rappuoli, Rio
APPLICANT: Rappuoli, Rio
APPLICANT: Rappuoli, Rio
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REPERENCE: CHICALOLS9
CURRENT APPLICATION UNUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PALENTIN UNIMBER: SCALENTING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PALENTING DATE: 1999-01-14
TYPE: PRICE TRING DATE: 1999-01-14
TYPE: PRICE TRING DATE: 1999-01-14
                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50664
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 VRERGPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 VRERGPQ 120
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7595
LENGTH: 274
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                                                                                                                                                                                                                                                               Sequence 2, Application US/09997165
; Patent No. 6762030
; GRNERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Fanslow, William C.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997,165
; CURRENT APPLICATION NUMBER: PCT/US00/14612
; PRIOR APPLICATION NUMBER: 60/1167
; PRIOR APPLICATION NUMBER: 60/1166
; PRIOR APPLICATION NUMBER: 60/1166
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
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Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches
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2.5%; Score 7; DB 4.
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7595, Application US/09489039A
Patent No. 6610836
; GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 50
US-09-270-767-35447
; Sequence 35447, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-997-165-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 NTLSSPN 140
                                        193 QEEIKEN 199
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                                                                                                             9 QEEIKEN 15
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US-09-489-039A-7595
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US-09-997-165-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE CP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 107196.132
CURRENT PAPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
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Sequence 6, Application US/08909125

Patent No. 6495737

Patent No. 6495737

APPLICANT: KLESSIG, DANIEL

APPLICANT: KLESSIG, DANIEL

APPLICANT: GUO, ALIAN

TITLE OF INVENTION: ALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANCE

TITLE OF INVENTION: ALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANCE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street

SILLE 720
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
  TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                    FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/418,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 173
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.5%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18251, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: CPn0171
US-09-438-185A-173
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Best Local Similarity 100.
Matches 7; Conservative
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STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ESSRSGH 257
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US-09-248-796A-18251
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Sequence 189, Application US/09198452A

Batent No. 6559294

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering Reference: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 189
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                                                OTHER INFORMATION: Description of Artificial Sequence: ORF114a
NAME/KEY: SITE
LOCATION: (58)
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APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Kalman,
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.5%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 90; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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8.09-438-185A-173
9.5equence 173, Application US/09438185A
Patent No. 6822071
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (179)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (114)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (209)
OTHER INFORMATION: place-holder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (344)...(355)
; OTHER INFORMATION: place-holder
US-09-302-626B-186
                                                                                                                           INFORMATION: place-holder
                                                                                                                                                                                                INFORMATION: place-holder
                                                                                                                                                                                                                                                                                                                      LOCATION: (139)
OTHER INFORMATION: place-holder
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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-189
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AAHITGT 129
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                                                                                                                        OTHER INFORMATIONAME/KEY: SITE LOCATION: (105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
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US-09-198-452A-189
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
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COUNTRY:

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GENERAL INC. 8012339

GENERAL INC. 8012339

GENERAL INC. 8012339

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-44-14

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESESEQ for Windows Version 4.0

SEQ ID NO 11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 628; . 1.3e+02; ches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5%; Score 7; DB 4
100.0%; Pred. No. 1.3
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11022, Application US/09949016 Patent No. 6812339
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; Sequence 34, Application US/09831642
; Patent No. 6635751
; GENERAL INFORMATION:
                                     DOCATION: (296)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
LOCATION: (343)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
LOCATION: (352)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
LOCATION: (377)
OTHER INFORMATION: place-holder
LOCATION: (417)
OTHER INFORMATION: place-holder
LOCATION: (417)
OTHER INFORMATION: place-holder
LOCATION: (447)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
LOCATION: (447)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
LOCATION: (447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (582)..(593)
; OTHER INFORMATION: place-holder US-09-302-626B-183
OTHER INFORMATION: place-holder
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAZE, Kyosuke et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.5
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 554; 1.2e+02;
                                                                               COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPAGE: SeatESQ Version 1.5
SOFTWARE: SeatESQ Version 1.5
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,125
FILING DATE: 11-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/024,033
FILING DATE: 12-AUG-1996
ATTORNEY AGENT INFORMATION:
NAME: JANET E. REED, PH.D.
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: ALEBORATION:
TELEPHONE: 215-563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maelgnani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIROLS
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT APPLICATION NUMBER: US/09/302,626B
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.5%; Score 7; DB of Best Local Similarity 100.0%; Pred. No. 1.3 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-302-626B-183
; Sequence 183, Application US/09302626B
; Patent No. 6709660
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (47)...(73)
OTHER INFORMATION: place-holder
NAME/KEY: SITE
LOCATION: (85)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                   ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 KALGRKI 483
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2.5%; Score 7; DB 4; Length 1532; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
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; Sequence 179, Application US/09302626B
; Parent No. 6708660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Rappidani, Vega
; APPLICANT: Rappidani, Rino
; APPLICANT: Rappidani, Rino
; APPLICANT: Grandi, Guido
                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (959)
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1270)
OTHER INFORMATION: unknown
NAME/KEY: SITE
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LOCATION: (1508)
OTHER INFORMATION: unknown
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; OTHER INFORMATION: unknown
US-09-302-626B-62
                                            LOCATION: (781)
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (963)..(965)
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1157)
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (1164)..(1165)
OTHER INFORMATION: unknown
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1175)..(1176)
OTHER INFORMATION: unknown
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LOCATION: (1220)..(1221)
OTHER INFORMATION: unknown
      OTHER INFORMATION: unknown
                                                                                     NAME/KEY: SITE
LOCATION: (805)
OTHER INFORMATION: unknown
NAME/KEY: SITE
                                                                                                                                                                        LOCATION: (903)
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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Best Local Similarity 100.
Matches 7; Conservative
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TITLE OF INVENTION: ENDOPLASMIC RETICULUM STRESS TRANSCRIPTION FACTORS ATF6 AND CREB-FILE REFERENCE: 1422-0474P
CURRENT APPLICATION WIMBER: US/09/031,642
CURRENT FILING DATE: 2011-05-11
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
LENGTH: 700
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                                                                                                                                                                                                                                                  Query Match 2.5%; Score 7; DB 4; Length 700; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-302-626B-62

Sequence 62, Application US/09302626B

Patent No. 6709660

GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Rappooli, Rino
APPLICANT: Rappooli, Rino
APPLICANT: Rappooli, Rino
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningcoccal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR APPLICATION DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (343)
OTHER INPORMATION: unknown
NAME/KEY: SITE
LOCATION: (352)
OTHER INFORMATION: unknown
NAME/KEY: SITE
LOCATION: (377)
OTHER INFORMATION: unknown
NAME/KEY: SITE
LOCATION: (417)
OTHER INFORMATION: unknown
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (68)..(73)
OTHER INPORMATION: unknown
NAME/KEY: SITE
LOCATION: (85)
OTHER INPORMATION: unknown
NAME/KEY: SITE
LOCATION: (296)
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (665)
OTHER INFORMATION: unknown
NAME/KEY: SITE
LOCATION: (693)..(694)
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INFORMATION: unknown
                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-09-831-642-34
                                                                                                                                                                                                                                                                                                                                                                     263 TVLLQSL 269
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LENGTH: 1532
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-13
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US-09-628-665-31
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Patent No. 6673771

GENERAL INFORMATION:

APPLICANT: Greene, Mark I.

APPLICANT: Kinosaki, Masahiko

TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity

FILE REFERENCE: UPN3831

CURRENT APPLICATION NUMBER: US/09/628,665

CURRENT FILING DATE: 1099-07-28

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIN Ver: 2.1

SEQ ID NO 31

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Greene, Mark I.
APPLICANT: Greene, Mark I.
APPLICANT: Kinosaki, Masahiko
TILE REPLICANT: Kinosaki, Masahiko
TILE REPLICANT: Kinosaki, Masahiko
FILE REFERENCE: UPN3831
CURRENT PEPLICATION NUMBER: US/09/628,665
CURRENT FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 6; DB 4; Length 6; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indelt
                                                                                                                                              DB 3; Ler
                                                                                                                                              2.5%; Score 7; DB 3
100.0%; Pred. No. 3.9
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     US-09-628-665-13; Sequence 13, Application US/09628665; Patent No. 6673771; Patent No. 6673771; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                    TYPE: PRT
; ORGANISM: Ashbya gossypii
US-09-415-522-6
                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                     137 SSPNSKN 143
                                                                                                                                                                                                                                                                  48 SSPNSKN 54
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       SEQ ID NO 6
LENGTH: 2071
                                                                                                                                                  Query Match
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Sequence 6, Application US/09415522A

GENERAL INFORMATION:

APPLICANT: Wendland, Juergen

APPLICANT: Philippsen, Peter

APPLICANT: Philippsen, Peter

TITLE OF INVENTION: Development

TITLE OF INVENTION: Development

FILE REPRENCE: CG22046

CURRENT PPLICATION WHMBER: US/09/415,522A

CURRENT FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 28
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US-09-302-626B-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 7; DB 4; Length 1978; 100.0%; Pred. No. 3.7e+02; arive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.5%; Score 7; DB 4; Length 1574; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60 Application US/09302626B

Sequence 60 Application US/09302626B

Patent No. 6709666

GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Pizza, Mariagrazia
APPLICANT: Fizza, Mariagrazia
APPLICANT: Pizza, Mariagrazia
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TILE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIROLS9
CURRENT PILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/1899/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PATENTING VET: 2.1
SEQ ID NO 60
LENGTH: 1978
TURENT: 1978
; TITLE OF INVENTION: Meningococcal Antigens; FILE REFERENCE: CHIR0159; CURRENT APPLICATION NUMBER: US/09/302,626B; CURRENT APPLICATION NUMBER: 1999-04-30; PRIOR APPLICATION NUMBER: PCT/IB99/00103; PRIOR FILING DATE: 1999-01-14; NUMBER OF SEQ ID NOS: 195; SEQ ID NO 179; SEQ ID NO 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 7; Conservative
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| 560 AAHITGT 566
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APPLICANT: Fraser, Jamet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: MINICAL) Particia J.
TITLE OF INVENTION: COMPOSITIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030, 619B
CURRENT PILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettee
COMPUTER: In Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Modgson, John
APPLICANT: Micholas, Bavid
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 6; DB 4;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Indolicidin Analogue US-09-030-619-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 268, Application US/08858207A
; Patent No. 6348328
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 46 amino acids TYPE: amino acid
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US-08-858-207A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: King
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Sequence 57665, Application US/09270767

Sequence 57665, Application US/09270767

Sequence 57665, Application US/09270767

GENERAL NO. 6703491

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: FILE REFERENCE: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 57665
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Jackson, W. James
APPLICANT: Jackson, W. James
APPLICANT: Pace, John
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
FILE REFERENCE: 1969-086-999
CURRENT APPLICATION NUMBER: US/09/612,402B
PRIOR APPLICATION NUMBER: 08/942,596
PRIOR PLING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
IENGTH: 24
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100.0%; Pred. No. ...
0; Mismatches
                     Pred. No. 35;
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100.0%; Pred. No. 79;
iive 0; Mismatches
                                           Mismatches
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                                                                                                                                                                                   RESULT 66
US-09-612-402B-26
; Sequence 26, Application US/09612402B
; Patent No. 6642023
100.08; Pre-
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; ORGANISM: Drosophila melanogaster
US-09-270-767-57665
                                         6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Chlamydia sp.
                                                                                157 SRSGHS 162
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Best Local Similarity
Matches 6; Conserv
                 Best Local Similarity
Matches 6; Conserv
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                                                                                                              3 SRSGHS 8
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Sequence 27194, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409
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GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PLIE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1909-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7381
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32209, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: HOMBURGE et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 32209
LENGTH: 76
LENGTH: 76
LENGTH: 76
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Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
1 LOCATION: 31
2 OTHER INFORMATION: Xaa=Glu or Lys
US-09-513-9990C-7381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%; Best Local Similarity 100.0%; Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 SNLHLR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AEYGLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AEYGLY 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 SNLHLR 30
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US-09-270-767-32209
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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APPLICANT: Gary L. Brecon et al.
APPLICANT: Gary L. Brecon et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6548
LENGTH: 62
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
SOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
LENGTH: 54
                                                                                                                                             Gaps
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                                                                                                                                          0; Indels
                                                                                             DB 3; Length 46; . 1.4e+02;
                                                                                             2.1%; Score 6; DB 3
100.0%; Pred. No. 1.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7381, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6548, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Acinetobacter baumannii
US-09-328-352-6548
  ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.00
Them 6; Conservative
                                                                                          Query Match 2.19
Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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19 FTNELK 24
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US-09-270-767-42298
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RESULT 72

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Search completed: June 22, 2005, 06:53:25
Job time : 45 secs
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21 NDEESM 26
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                      2.1%; Score 6; DB 4; Length 76;
100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: usa.
TIP: 0254
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COPERATING SYSTEM: <UNKNOWN>
SOCTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1017 2, 1997
ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
RECISTRATION NUMBER: 40,489
RECISTRATION NUMBER: 40,489
RECISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPOMUNICATION INFORMATION:
TYPE: amino acid
MYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...78
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5502:
US-09-107-532A-5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5502, Application US/09107532A; Patent No. 6583275; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
, PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27194
; LENGTH: 76
; TYPE: PRT
                                                                                                                            ; ORGANISM: Candida albicans
US-09-248-796A-27194
                                                                                                                                                                                                        Query Match 2.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                          24 VLLOSL 29
                                                                                                                                                                                                                                                                                                                                                  36 VLLQSL 41
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